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Remarks:

- The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.
- Claims 11 to 12 are deemed to be abandoned due to non-payment of the claims fees (Rule 31 (2) EPC).

(54) **Gastric helicobacter 16 S rDNA sequences from cattle and pigs and their use for detection and typing of Helicobacter strains**

(57) The present invention relates to new *Helicobacter* 16S rRNA or rDNA polynucleotide sequences useful for detection and typing of *Helicobacter* infected human and animal samples. The present invention relates more particularly to new "*Candidatus Helicobacter bovis*" and "*Candidatus Helicobacter suis*" sequences

as defined in SEQ ID NO 1 and 2, sequence variants and fragments thereof. These new *Helicobacter* sequences allow the design of sequence specific probes and primers for detection and typing of the strains they are derived from. Diagnostic methods and kits employing such new bovine and porcine *Helicobacter* sequences are also disclosed.

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## Description

[0001] The present invention relates to the field of detection and typing of *Helicobacter* infection in clinical samples from humans and other mammals. The present invention relates more particularly to bovine and porcine 16 rDNA polynucleotide sequences as well as their use in diagnostic applications.

[0002] In the 19<sup>th</sup> century, gastric spiral organisms were described for the first time in different animals (Rappin, 1881; Bizzozero, 1893; Salomon, 1896). Salomon observed spiral organisms in the stomachs of dogs, cats and the brown Norwegian rat but not in humans, monkeys, pigs, mice, pigeons, crows and cattle (Salomon, 1896). It was only in 1984 that a renewed interest emerged for similar organisms after the isolation of *Helicobacter pylori* from the human stomach (Marshall & Warren, 1984). The association of *H. pylori* with chronic gastritis, peptic ulceration and gastric cancer (Cover & Blaser, 1992; Blaser et al., 1991; Parsonnet et al., 1991) resulted in intensive research worldwide. Various *Helicobacter* species were isolated from the gastrointestinal tract of different animals. To date, the genus *Helicobacter* consists of 18 different species (On, 1996; Franklin et al., 1996; Mendes et al., 1996; Jalava et al., 1997; Trivett-Moore et al., 1997; Shen et al., 1997) and constitutes together with the genera *Wolinella*, *Campylobacter* and *Arcobacter*, the epsilon subdivision of the *Proteobacteria*, also known as rRNA superfamily VI (Vandamme et al., 1991).

[0003] In 1992, two different groups almost simultaneously reported the presence of helically shaped bacteria in the abomasum of calves and adult cattle based on histological data (Günther & Schulze, 1992; Haringsma & Mouwen, 1992). Both groups described large numbers of spiral-shaped bacteria in the gastric crypts of the pyloric region and considered them as putative *Helicobacter* species. Further indirect evidence of the presence of *Helicobacter*-like organisms in adult cattle and calves was given by serological studies. Seidel et al. (1996) found significant titers of antibodies against *H. pylori* epitopes in the serum of calves after absorption with *Campylobacter jejuni*, *Wolinella succinogenes*, *Escherichia coli* and *Proteus mirabilis* strains. One report described a bactericidal activity of bovine serum, colostrum and milk against *H. pylori* (Korhonen et al., 1995). In vitro isolation of these organisms has not been successful so far (Jeilinski et al., 1995; Braun et al., 1997) and the taxonomic status of these putative *Helicobacter*-like bacteria is unknown.

[0004] The pathogenic role of *H. pylori* led to speculations about the association of bovine *Helicobacter*-like bacteria with abomasal ulcer disease, although no conclusive evidence has been provided to date (Günther & Schulze, 1992; Haringsma & Mouwen, 1992). Other bacteria such as *Campylobacter* species and *Clostridium perfringens* have also been studied in association with the occurrence of abomasal lesions (Al Mashat & Taylor, 1980; Mills et al., 1990; Jeilinski et al., 1995).

[0005] Within the genus *Helicobacter*, a phylogenetic subgroup of morphologically similar bacteria can be distinguished. These bacteria, characterized by their long and tightly coiled (gastrospirillum-like) appearance, have been observed in gastric biopsies of humans, cats, lemurs, dogs, pigs and exotic carnivores (Dent et al., 1987; Lee et al., 1988; O'Flourke et al., 1992; Hänninen et al., 1996; Jalava et al., 1997; Queiroz et al., 1990; Eaton et al., 1993; Jakob et al., 1997). Three species with this morphology (*H. felis*, *H. bizzozeronii*, *H. salomonis*) have been isolated and characterised from gastric samples of cats and dogs (Paster et al., 1991; Hänninen et al., 1996; Jalava et al., 1997).

[0006] The observation of gastrospirillum-like organisms in humans was described for the first time in 1987 by Dent et al. (Dent et al., 1987). Although initially referred to as "*Gastrospirillum hominis*" (McNulty et al., 1989), this organism was later renamed "*Helicobacter heilmannii*" as 16S rDNA sequence analysis revealed that these human gastrospirilla belonged to the genus *Helicobacter* (O'Flourke et al., 1992; Solnick et al., 1993). From these results, it also became clear that there were at least two different types of "*Helicobacter heilmannii*", referred to as type 1 and type 2. This observation was based on a 3.5 % sequence difference, suggesting that the two sequences represented two different species. The first isolation of a "*Helicobacter heilmannii*"-like bacterium from humans was recently reported by Andersen et al. (1996).

[0007] In pigs, gastrospirillum-like bacteria were observed in the antral pits and at the mucosal surface of the stomach (Queiroz et al., 1990) and have provisionally been named "*Gastrospirillum suis*" (Mendes et al., 1990). Histopathological studies associated this bacterium with pyloric lymphonodular gastritis (Mendes et al., 1991) and gastric ulcer disease of the pars oesophagea in pigs (Barbosa et al., 1995; Queiroz et al., 1996). Although *in vitro* cultivation of "*Gastrospirillum suis*" has been unsuccessful (Queiroz et al., 1990), *in vivo* cultivation in mice and rats has been reported (Moura et al., 1993; Mendes et al., 1996). In one case, a *Helicobacter* was isolated from the faeces of swine (Seymour et al., 1994) which was later characterised as *Helicobacter pametensis* (Dewhirst et al., 1994). Other members of rRNA superfamily VI, *Campylobacter hyointestinalis* subsp. *Lawsonii* (On et al., 1995), *Arcobacter butzleri* and *Arcobacter cryaerophilus* (Suarez et al., 1997), have also been isolated from the stomach of swine.

[0008] As "*Gastrospirillum suis*" remains unculturable, an official species designation is impossible according to the guidelines of the International Code of Nomenclature of Bacteria which are stating the necessity of a broad range of phenotypic and phylogenetic data. Murray and Schleifer (1994) anticipated this problem, and proposed a provisional status to record the properties of putative taxa of prokaryotes. This proposal was implemented in 1995 by the International Committee on Systematic Bacteriology by the introduction of the provisional status *Candidatus* for the description

of uncultivable organisms based upon genomic data and to a certain extent structural, metabolic, reproductive and environmental characteristics [Murray and Stackebrandt, 1995].

[0009] It is an aim of the present invention to provide new *Helicobacter* nucleotide sequences of the 16S rRNA coding gene.

[0010] It is also an aim of the present invention to provide new probes and primers for detection of *Helicobacter* species.

[0011] It is also an aim of the present invention to provide methods and kits for detection and/or typing of *Helicobacter* species present in cattle and pigs.

[0012] It is further an aim of the present invention to provide methods and kits for detection of *zoönoses* in human samples.

[0013] It is also an aim of the present invention to provide new nucleotide sequences for studying and detecting the occurrence of pathogenic *Helicobacter* strains in mammals, more particularly in cattle and pigs.

[0014] All the aims of the present invention are met by the following embodiments.

[0015] According to one embodiment, the present invention relates to an isolated 16S rDNA *Helicobacter* polynucleic acid sequence selected from any of the following

(a) a sequence represented in any of SEQ ID NO 1 or 2, or the RNA version thereof,

(b) a sequence which hybridizes under stringent conditions to any of the sequences set out in (a).

[0016] The term "16S ribosomal polynucleic acid sequences" as used in the present invention refers to 16S rRNA or 16S rDNA polynucleic acid sequences.

[0017] According to a first aspect of the present invention, seven abomasal biopsies of adult cattle were sampled from different Belgian and Dutch farms. In all samples the presence of *Helicobacter*-like organisms was demonstrated by biochemical, immunohistochemical and electronmicroscopical data. Bacterial 16S rDNA was amplified from each sample by PCR and sequences were determined either by direct or indirect sequence analysis. Pairwise comparisons revealed all sequences to be more than 99 % homologous. Phylogenetic analysis placed the organism, corresponding to the reference sequence R2XA, within the genus *Helicobacter*. A diagnostic PCR-assay was designed, differentiating the bovine 16S rDNA sequences from those of 15 different *Helicobacter* strains and *Wolinella succinogenes*. These results indicated the corresponding organism to represent a single taxon. The low similarity level towards *H. bilis* (92.8 %), its closest validly named neighbour, strongly suggests that this novel taxon indeed is a novel *Helicobacter* species. An *in situ* hybridisation procedure associated the bovine sequences to the *Helicobacter*-like organisms in the abomasum.

[0018] According to a second aspect, the present invention relates to new *Helicobacter* sequences from pigs. Stomachs of five slaughterhouse pigs originating from different Belgian and Dutch farms were selected based on the presence of "*Gastrosprillum suis*"-like bacteria as demonstrated by biochemical, immunohistochemical and electronmicroscopical data. Using broad range primers, bacterial 16S rDNA was amplified by PCR and five *Helicobacter*-like sequences were determined either by direct or indirect sequence analysis. An intersequence homology of 99.7 % was observed, suggesting that the sequences originated from strains belonging to a single species. Phylogenetic analysis of the consensus sequence placed the organism within the genus *Helicobacter*, where it formed a distinct subgroup together with other gastrosprillum-like bacteria (*H. felis*, *H. bizzozeronii*, *H. salomonis*, "*H. heilmannii*" type 1 and type 2). Diagnostic PCR-primers and a probe were developed, differentiating the porcine sequences from all known *Helicobacters*. These results indicate that the porcine sequences represent a single taxon within the genus *Helicobacter*. The low similarity level towards *H. salomonis* (96.6 %), its closest validly named neighbour, strongly suggests that this novel taxon indeed is a novel *Helicobacter* species. *In situ* hybridisation experiments linked the reference sequence to the "*Gastrosprillum suis*"-like bacteria. On the basis of these results, the name "*Candidatus Helicobacter suis*" for this new gastric *Helicobacter* from pigs is proposed.

[0019] These sequences are commonly characterized by the fact that they can be used to study and most probably detect pathogenic *Helicobacter* strains in mammals, more particularly in cattle and pigs. Such pathogenic strains cause for instance gastric ulcers and chronic gastritis.

[0020] The present invention relates more particularly to an isolated polynucleic acid sequence as defined above represented by any of SEQ ID NO 1 or 2 or 15 to 24.

[0021] The present invention also relates to an isolated polynucleic acid sequence as defined above which is more than 92.8%, preferably more than 93.5%, more preferably more than 95% and most preferably more than 97.5% homologous to SEQ ID NO 1. Other preferred ranges of homology include 93, 94, 94.5, 95.5, 96, 96.5, 97, 98, 98.5, 99 or 99.5%.

[0022] Sequences which have a homology of more than 92.8% to SEQ ID NO 1 are considered to belong to the same group of organisms as the one where SEQ ID NO 1 has been derived from.

[0023] According to the present invention, the homologies of SEQ ID NO 1 were calculated by means of the GENSCAN program (Applied Maths bvba, Risquons-toutstraat 38, B-8511 Kortrijk, Belgium).

[0024] The term "homology" refers to a sequence identity as calculated by the above-given program.

[0025] SEQ ID NO 2 is 99.5% homologous to the closest found sequence. Sequences of more than 99.5% homology compared to SEQ ID NO 2 are also within the scope of the present invention.

[0026] Preferred sequences according to the present invention are set out in Figures 1, 2, 4 and 5: SEQ ID NO 1 to 2 and 15 to 24. Also unique parts and fragments of these sequences are part of the present invention. Preferred unique parts are set out in Table 2.

[0027] Since SEQ ID NO 2 shows 96.6% homology to its closest found validly named neighbour, the use of sequences of more than 96.6% homology to SEQ ID NO 1 for identification or typing of *Helicobacter* species is also within the scope of the present invention. Preferably sequences of more than 97%, 97.5%, 98%, 98.5%, 99% or 99.5% homology to SEQ ID NO 2 are used for this goal.

[0028] According to another embodiment, the present invention relates to a part of an isolated polynucleic acid as defined above, more particularly part or a fragment of SEQ ID NO 1 or 2, wherein said part is unique to the polynucleic acid sequence it is derived from.

[0029] According to the present invention, the term "unique" implies that at least one nucleotide of the fragment or part is different from a nucleotide present at the same nucleotide position in a known 16S rRNA sequence or the corresponding gene. Such a nucleotide can be deduced theoretically by looking at an alignment of the new sequences of this invention with other closely related *Helicobacter* 16S rDNA gene nucleotide sequences (see Figures 1, 2, 4 and 5). Said type of nucleotides are unique to the sequence they are derived from. These fragments are thus not part of any known 16S rRNA or gene sequence encoding the same. The fragments according to this embodiment of the present invention may be of any length between 10 to the maximum number of nucleotides of SEQ ID NO 1 or 2 or its variants. Preferred lengths are 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, etc. nucleotides.

[0030] According to another embodiment, the present invention relates to a probe which specifically hybridizes to a polynucleic acid sequence as defined above.

[0031] Preferred probes are given in Table 2. Probe R628f is a preferred "*Candidatus Helicobacter bovis*" specific probe. Probe V100f is a preferred "*Candidatus Helicobacter suis*" specific probe. Other suitable probes may be derived from a visual inspection of the alignment shown in Figure 1 or 2.

[0032] According to another embodiment, the present invention relates to a primer which specifically amplifies a polynucleic acid sequence as defined above.

[0033] Preferred primers according to the present invention are given in Table 2. Primers R574f and R832r are preferred "*Candidatus Helicobacter bovis*" specific primers and are suited for a specific PCR and in situ hybridisation assays. Primers V832f and V1621r are preferred "*Candidatus Helicobacter suis*" specific primers for a specific PCR and in situ hybridisation assays. Other suitable primers according to the present invention may be derived from a visual inspection of the alignment shown in Figure 1 or 2.

[0034] Relying on the principles well known in the art, the skilled man will be able to select primers that allow specific amplification of SEQ ID NO 1 or 2 or the claimed variants thereof under given or experimental conditions, such as temperature, buffer composition, polymerase chain reaction cycle etc. Likewise the skilled man will be able to select probes that specifically hybridize to either SEQ ID NO 1 or 2 or the claimed variants under given experimental conditions such as temperature, buffer composition etc. Having chosen primers and/or probes, the skilled man will furthermore be able to assess the efficacy of these primers or probes without undue experimentation. It is also obvious that the skilled man may choose to combine more than one primer pair or more than one probe to carry out the method defined above.

[0035] In some cases, one may not wish to detect all SEQ ID NO 1 or 2 variants as specified above, for instance if one intends to detect alleles found in a certain geographic region.

[0036] According to another embodiment, the present invention relates to a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising hybridizing the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one probe as defined above.

[0037] Preferably said method may be used to study and detect the occurrence of pathogenic *Helicobacter* strains.

[0038] According to another embodiment, the present invention relates to a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically amplifying the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one primer as defined above.

[0039] Preferably said method may be used to study and detect the occurrence of pathogenic *Helicobacter* strains.

[0040] A preferred embodiment according to the present invention involves a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising first amplifying a specific target region encompassed in or comprising the 16S rRNA region of said *Helicobacter* strains present in said biological sample and subsequently hybridizing the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said bio-

logical sample with at least one (or more than one) probe as defined above.

[0041] Different techniques can be applied to perform the methods of the present invention. These techniques may comprise immobilizing the target polynucleic acids, possibly after amplification, on a solid support and performing a hybridization with labelled oligonucleotide probes of the present invention. Alternatively, said probes may be immobilized on a solid support and hybridization may be performed with labelled target polynucleic acids, possibly after amplification (i.e. a reverse hybridization).

[0042] A preferred method according to the present invention is an *in situ* hybridisation assay (see Examples section).

[0043] The well-known technique of Southern blotting is one example of a hybridization assay that can be used to perform the methods of the present invention. Another example of a hybridization technique is the DNA enzyme immuno assay (DEIA). According to this method, PCR products are generated by a primer set, of which either the forward or the reverse primer contain biotin at the 5' end. This allows binding of the biotinylated amplimers to streptavidin-coated microtiter wells. PCR products are denatured by sodium hydroxide, which allows removal of the non-biotinylated strand. Specific digoxigenin (DIG)-labelled oligonucleotide probes are hybridized to the single-stranded immobilized PCR product and hybrids are detected by enzyme-labelled conjugate and colorimetric methods.

[0044] A convenient reverse hybridization technique is the LiPA assay. The LiPA uses oligonucleotide probes immobilized as parallel lines on a solid support strip (Stuyver et al. 1993; international patent application WO 94/12670). This approach is particularly advantageous since it is fast and simple to perform.

[0045] It is to be understood that any other type of hybridization assay or hybridization format using any of the selected probes as described further in the invention, is also covered by the present invention.

[0046] According to another embodiment, the present invention relates to a diagnostic kit for detection and/or typing of *Helicobacter* strains comprising:

- at least one probe as defined above and/or,

- at least one primer as defined above.

[0047] According to another embodiment, the present invention relates to a medicament comprising a polynucleic acid sequence as defined above.

[0048] According to another embodiment, the present invention relates to a polynucleic acid sequence as defined above for use as a medicament.

[0049] The following definitions and explanations will permit a better understanding of the present invention.

[0050] The target material in the samples to be analysed may either be DNA or RNA, e.g. genomic DNA, messenger RNA, viral RNA or amplified versions thereof. These molecules are in this application also termed "polynucleic acids" or "polynucleotides". More particularly, the target material according to the present invention will be 16S ribosomal RNA or DNA or amplified versions thereof.

[0051] Well-known extraction and purification procedures are available for the isolation of RNA or DNA from a sample (e.g. in Sambrook et al., 1989).

[0052] The term "probe" according to the present invention refers to a single-stranded oligonucleotide which is designed to specifically hybridize to "*Candidatus Helicobacter bovis* or *suis*" polynucleic acids.

[0053] The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products. Preferably the primer is about 5-50 nucleotides long. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions at which the primer is used, such as temperature and ionic strength. It is to be understood that the primers of the present invention may be used as probes and vice versa, provided that the experimental conditions are adapted.

[0054] The expression "suitable primer pair" in this invention refers to a pair of primers allowing specific amplification of a "*Candidatus Helicobacter bovis* or *suis*" polynucleic acid fragment.

[0055] The term "target region" of a probe or a primer according to the present invention is a sequence within the "*Candidatus Helicobacter bovis* or *suis*" polynucleic acids to which the probe or the primer is completely complementary or partially complementary (i.e. with some degree of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

[0056] "Specific hybridization" of a probe to a target region of respectively the "*Candidatus Helicobacter bovis*" or "*Candidatus Helicobacter suis*" polynucleic acids means that said probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions said probe does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

[0057] "Specific hybridization" of a primer to a target region of respectively the "*Candidatus Helicobacter bovis*" or "*Candidatus Helicobacter suis*" polynucleic acids means that, during the amplification step, said primer forms a duplex

with part of this region or with the entire region under the experimental conditions used, and that under those conditions said primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

[0058] "Specific amplification" of a fragment of respectively the "*Candidatus Helicobacter bovis*" or "*Candidatus Helicobacter suis*" polynucleic acids means amplification of the fragment for which the primers were designed, and not of any other fragment of the polynucleic acids present in a sample.

[0059] The fact that amplification primers do not have to match exactly with the corresponding target sequence in the template to warrant proper amplification is amply documented in the literature (Kwok et al., 1990). However, when the primers are not completely complementary to their target sequence, it should be taken into account that the amplified fragments will have the sequence of the primers and not of the target sequence. Primers may be labelled with a label of choice (e.g. biotine). The amplification method used can be either polymerase chain reaction (PCR, Saiki et al., 1988), ligase chain reaction (LCR; Landgren et al., 1988; Wu & Wallace, 1989; Barany, 1991), nucleic acid sequence-based amplification (NASBA; Guatelli et al., 1990; Compton, 1991), transcription-based amplification system (TAS; Kwok et al., 1989), strand displacement amplification (SDA; Duck, 1990) or amplification by means of Q $\beta$  replicase (Lormeli et al., 1989) or any other suitable method to amplify nucleic acid molecules known in the art.

[0060] Preferably, the probes of the invention are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides. Particularly preferred lengths of probes include 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics.

[0061] Probe and primer sequences are represented throughout the specification as single stranded DNA oligonucleotides from the 5' to the 3' end. It is obvious to the man skilled in the art that any of the below-specified probes can be used as such, or in their complementary form, or in their RNA form (wherein T is replaced by U).

[0062] The probes according to the invention can be prepared by cloning of recombinant plasmids containing inserts including the corresponding nucleotide sequences, if need be by excision of the latter from the cloned plasmids by use of the adequate nucleases and recovering them, e.g. by fractionation according to molecular weight. The probes according to the present invention can also be synthesized chemically, for instance by the conventional phospho-triester method.

[0063] The oligonucleotides used as primers or probes may also comprise nucleotide analogues such as phosphorothiates (Matsukura et al., 1987), alkylphosphorothiates (Miller et al., 1979) or peptide nucleic acids (Nielsen et al., 1991; Nielsen et al., 1993) or may contain intercalating agents (Asseline et al., 1984). As most other variations or modifications introduced into the original DNA sequences of the invention these variations will necessitate adaptations with respect to the conditions under which the oligonucleotide should be used to obtain the required specificity and sensitivity. However, the eventual results of hybridization will be essentially the same as those obtained with the unmodified oligonucleotides. The introduction of these modifications may be advantageous in order to positively influence characteristics such as hybridization kinetics, reversibility of the hybrid-formation, biological stability of the oligonucleotide molecules, etc.

[0064] The term "solid support" can refer to any substrate to which an oligonucleotide probe can be coupled, provided that it retains its hybridization characteristics and provided that the background level of hybridization remains low. Usually the solid substrate will be a microtiter plate, a membrane (e.g. nylon or nitrocellulose) or a microsphere (bead) or a chip. Prior to application to the membrane or fixation it may be convenient to modify the nucleic acid probe in order to facilitate fixation or improve the hybridization efficiency. Such modifications may encompass homopolymer tailing, coupling with different reactive groups such as aliphatic groups, NH<sub>2</sub> groups, SH groups, carboxylic groups, or coupling with biotin, haptens or proteins.

[0065] The term "labelled" refers to the use of labelled nucleic acids. Labelling may be carried out by the use of labelled nucleotides incorporated during the polymerase step of the amplification such as illustrated by Saiki et al. (1988) or Bej et al. (1990) or labelled primers, or by any other method known to the person skilled in the art. The nature of the label may be isotopic (<sup>32</sup>P, <sup>35</sup>S, etc.) or non-isotopic (biotin, digoxigenin, etc.).

[0066] The "biological sample" may be for instance cultured *Helicobacter* strains, gastric, abomasal stomachs, omasal stomachs, reticulum and rumen, or duodenal biopsies (fresh or paraffine material), faeces, saliva, mouth mucosa, gastric juice or urine. Preferably these samples may be taken from piglets, pigs, humans, calves, cattle, etc.

[0067] For designing probes with desired characteristics, the following useful guidelines known to the person skilled in the art can be applied.

[0068] Because the extent and specificity of hybridization reactions such as those described herein are affected by a number of factors, manipulation of one or more of those factors will determine the exact sensitivity and specificity of a particular probe, whether perfectly complementary to its target or not. The importance and effect of various assay conditions are explained further herein.

[0069] \*\*The stability of the [probe : target] nucleic acid hybrid should be chosen to be compatible with the assay

conditions. This may be accomplished by avoiding long AT-rich sequences, by terminating the hybrids with G-C base pairs, and by designing the probe with an appropriate T<sub>m</sub>. The beginning and end points of the probe should be chosen so that the length and %GC result in a T<sub>m</sub> about 2-10°C higher than the temperature at which the final assay will be performed. The base composition of the probe is significant because G-C base pairs exhibit greater thermal stability as compared to A-T base pairs due to additional hydrogen bonding. Thus, hybridization involving complementary nucleic acids of higher G-C content will be more stable at higher temperatures.

[0070] \*\*Conditions such as ionic strength and incubation temperature under which a probe will be used should also be taken into account when designing a probe. It is known that the degree of hybridization will increase as the ionic strength of the reaction mixture increases, and that the thermal stability of the hybrids will increase with increasing ionic strength. On the other hand, chemical reagents, such as formamide, urea, DMSO and alcohols, which disrupt hydrogen bonds, will increase the stringency of hybridization. Destabilization of the hydrogen bonds by such reagents can greatly reduce the T<sub>m</sub>. In general, optimal hybridization for synthetic oligonucleotide probes of about 10-50 bases in length occurs approximately 5°C below the melting temperature for a given duplex. Incubation at temperatures below the optimum may allow mismatched base sequences to hybridize and can therefore result in reduced specificity.

[0071] \*\*It is desirable to have probes which hybridize only under conditions of high stringency. Under high stringency conditions only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. The degree of stringency is chosen such as to maximize the difference in stability between the hybrid formed with the target and the non-target nucleic acid.

[0072] \*\*Regions in the target DNA or RNA which are known to form strong internal structures inhibitory to hybridization are less preferred. Likewise, probes with extensive self-complementarity should be avoided. As explained above, hybridization is the association of two single strands of complementary nucleic acids to form a hydrogen bonded double strand. It is implicit that if one of the two strands is wholly or partially involved in a hybrid that it will be less able to participate in formation of a new hybrid. There can be intramolecular and intermolecular hybrids formed within the molecules of one type of probe if there is sufficient self complementarity. Such structures can be avoided through careful probe design. By designing a probe so that a substantial portion of the sequence of interest is single stranded, the rate and extent of hybridization may be greatly increased. Computer programs are available to search for this type of interaction. However, in certain instances, it may not be possible to avoid this type of interaction.

[0073] \*\*Standard hybridization and wash conditions are disclosed in the Examples section. Other conditions are for instance 3X SSC (Sodium Saline Citrate), 20% deionized FA (Formamide) at 50°C. Other solutions (SSPE (Sodium saline phosphate EDTA), TMAC (Tetramethyl ammonium Chloride), etc.) and temperatures can also be used provided that the specificity and sensitivity of the probes is maintained. When needed, slight modifications of the probes in length or in sequence have to be carried out to maintain the specificity and sensitivity required under the given circumstances. [0074] The term "hybridization buffer" means a buffer allowing a hybridization reaction between the probes and the polynucleic acids present in the sample, or the amplified products, under the appropriate stringency conditions.

[0075] The term "wash solution" means a solution enabling washing of the hybrids formed under the appropriate stringency conditions.

[0076] The Examples as set out below only serve to illustrate the present invention. The contents of all references referred to in this text are hereby incorporated by reference.

## FIGURE AND TABLE LEGENDS

### [0077]

Figure 1 represents an alignment of the reference sequence R2XA of "*Candidatus Helicobacter bovis*" (SEQ ID NO 1) with sequences of strains belonging to the epsilon subdivision (Table 3) which were retrieved from the EMBL data library and were aligned with reference sequence R2XA

Figure 2 represents an alignment of the reference sequence V2BXA of "*Candidatus Helicobacter suis*" (SEQ ID NO 2) sequence with the sequences of strains belonging to the same phylogenetic lineage (Table 3).

Figure 3A represents a phylogenetic tree based on the phylogenetic analysis of "*Candidatus Helicobacter bovis*" as set out in the Examples section. The scale bar represents a one % difference in nucleotide sequences as determined by measuring the length of horizontal lines connecting any two species.

Figure 3B represents a phylogenetic tree based on the phylogenetic analysis of "*Candidatus Helicobacter suis*" as set out in the Examples section. The scale bar represents a one % difference in nucleotide sequences as determined by measuring the length of horizontal lines connecting any two species.

Figure 4 represents an alignment of the different "*Candidatus Helicobacter bovis*" sequences. The reference sequence is R2XA001 (SEQ ID NO 1). The other sequences are R5XE001 (SEQ ID NO 15), R3XA001 (SEQ ID NO 16), R6XA001 (SEQ ID NO 17), R13D001INV (SEQ ID NO 18), R27TOTAAL (SEQ ID NO 19) and R28TOTAAL (SEQ ID NO 20).

Figure 5 represents an alignment of the different "*Candidatus Helicobacter suis*" sequences. The reference sequence is RBXA001 (SEQ ID NO 2). The other sequences are 4AXA001 (SEQ ID NO 21), 6W06001 (SEQ ID NO 22), V14D001 (SEQ ID NO 23), V19DINV001 (SEQ ID NO 24).

## EXAMPLES

### Material and Methods

#### Samples from cattle

[0078] Seven abomasal stomachs from clinically healthy slaughterhouse cattle originating from different Belgian and Dutch farms, were selected. The stomachs were opened longitudinally along the greater curvatura and rinsed gently with tap water. Two small mucosal fragments were taken from each stomach, one near the torus pyloricus and one in the fundic region, and were tested for urease activity (CUTest, Temmler Pharma) for 1 h at 37 °C. Three mucosal biopsies from the pyloric region were taken for immunohistochemistry and *in situ* hybridisation and placed into 4 % buffered formalin for 24 hours. For electronmicroscopy, a pyloric sample was taken from the same region and fixed in cacodylate buffer (0.1 M, pH 7.0) containing 5 % glutaraldehyde and 0.15 % (wt/vol) ruthenium red. From each stomach a mucosal fragment was also taken for PCR analysis, placed into sterile PBS and frozen in liquid nitrogen. Special care was taken during sampling to avoid cross-contamination.

#### Samples from pigs

[0079] Stomachs from 5 healthy slaughterhouse pigs were selected, all originating from different farms in Belgium and the Netherlands. The stomachs were opened longitudinally along the greater curvatura and rinsed gently with tap water. A small mucosal fragment was taken from each stomach near the torus pyloricus and placed into an urease test tube (CUTest, Temmler Pharma) for 2 hours at 37 °C. Mucosal biopsies from the antral part of the stomach were taken along the curvatura major ( $n=2$ ) and the curvatura minor ( $n=2$ ) for immunohistochemical evaluation and placed into 4 % buffered formalin. For electronmicroscopy, samples were taken from the same places and fixed in 0.1 M cacodylate buffer (pH 7.0) containing 5 % glutaraldehyde and 0.15 % (wt/vol) ruthenium red. Of each stomach a mucosal fragment was also taken for PCR, placed into sterile PBS and frozen in liquid nitrogen. Special care was taken during sampling to avoid cross-contamination.

#### Reference strains for "*Candidatus Helicobacter bovis*"

[0080] A total of 15 *Helicobacter* strains and 1 *Wolinella succinogenes* strain were used to test the specificity of the "*Candidatus Helicobacter bovis*" specific PCR (Table 1). Strains were grown on a 5 % Mueller-Hinton blood agar and incubated at 37 °C in a microaerophilic atmosphere containing approximately 5 % O<sub>2</sub>, 3.5 % CO<sub>2</sub>, 7.5 % H<sub>2</sub> and 84 % N<sub>2</sub>. Bacteriological purity was checked by plating and Gram-staining.

#### Reference strains for "*Candidatus Helicobacter suis*"

[0081] A total of 15 *Helicobacter* strains were used to test the specificity of the "*Candidatus Helicobacter suis*"-specific PCR assay (Table 1). Strains were grown on a 5 % Mueller-Hinton blood agar and incubated at 37 °C in a microaerobic atmosphere containing approximately 5 % O<sub>2</sub>, 3.5 % CO<sub>2</sub>, 7.5 % H<sub>2</sub> and 84 % N<sub>2</sub>. Bacteriological purity was checked by plating and Gram-staining.

#### Immunohistochemistry

[0082] Immunohistochemical staining was performed to assess the presence of *Helicobacter*-like organisms. Formalin-fixed samples were dehydrated and paraffin-embedded. Sections of 4 µm were made of the paraffin-embedded tissues and were placed on 3-aminopropyltriethoxysilane-coated slides (APES, Sigma-Aldrich) and dried overnight at 60 °C. After dewaxing with xylene and rehydration in graded series with ethanol and distilled water, sections were placed in citrate buffer (0.1M with 2% ureum) and were boiled (1 x 3 min, 2 x 5 min) in a 800 Watt microwave oven



(Whirlpool M611) to elicit antigen retrieval. Slides were then incubated with 12 % hydrogen peroxide in methanol (30 min) in order to block endogenous peroxidase activity. Thereafter the slides were pre-incubated with 30 % normal goat serum in PBS for 30 min to reduce non-specific antibody binding. A mouse polyclonal antibody directed against *H. pylori* (DAKO), diluted 1/20 in PBS, was incubated overnight at 21 °C in a moist chamber. The sections were washed and incubated with biotinylated swine anti-rabbit immunoglobulins at 21 °C for 30 min and after rinsing covered with peroxidase conjugated streptavidin-biotin-complex (ABC). Peroxidase activity was developed using H<sub>2</sub>O<sub>2</sub> with diaminobenzidine (DAB) as a chromogen (Fast DAB Tablet Set, Sigma-Aldrich). Subsequently, the sections were counterstained with Mayer's hematoxylin and mounted. As a negative control, the primary antibody was replaced with fetal calf serum in Tris-HCl buffer (pH 7.6). As a positive control, a section of a mouse stomach experimentally infected with *Helicobacter pylori* LMG 7539<sup>T</sup> was used.

#### Transmission electronmicroscopy

[0083] For "*Candidatus Helicobacter bovis*", three different pyloric samples were selected for electronmicroscopic evaluation based upon the high presence of *Helicobacter*-like organisms in the corresponding immunostained sections. [0084] For "*Candidatus Helicobacter suis*", two different antral biopsies were selected for electronmicroscopic evaluation based on the high presence of gastrosprillum-like organisms in the corresponding immunostained slides. [0085] After dehydration in a graded series of acetone washes, the samples were embedded in Spurr low-viscosity resin. Ultrathin sections were poststained with uranyl acetate and lead citrate and examined with an electronmicroscope (Phillips 201 TEM) at an accelerating voltage of 60 kV.

#### DNA-extraction

[0086] DNA was isolated from the scrapings of the gastric biopsies and from the reference strains by lysis with guanidinium isothiocyanate and DNA was bound to silica particles according to the method of Boom et al. (1990).

#### Primers and PCR amplification of 16S rDNA

[0087] Broadrange primers *H33f*, *H61f* and *H1368r* were selected from rRNA superfamily VI (*Helicobacter*, *Campylobacter*, *Arcobacter*, *Wolinella*) specific regions of the 16S rRNA gene (Table 2).

[0088] The use of broad range primer *1492RPL* was suggested by Weissburg et al. (1991). A genus *Helicobacter*-specific primer *H274f* was adapted from primer *274r* described by Dewhirst et al. (1994) (Table 2). Primer combinations *H33f-H1368r*, *H274f-1492RPL* and *H61f-1492RPL* were used to amplify a ~ 1.3-Kb, ~ 1.2-Kb and a ~ 1.4-Kb fragment of "*Candidatus Helicobacter suis*" respectively.

[0089] PCR reactions were performed in a volume of 50 µl containing 10mM Tris HCl (pH 8.3), 50 mM KCl, 3.5 mM MgCl<sub>2</sub>, 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold (Perkin-Elmer, Roche Molecular Systems) and 25 pmol of both forward and reverse primer (Eurogentec). Reactions were covered with mineral oil and PCR was performed in a Biomed-60 thermocycler under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 50 cycles of 30 s at 94 °C, 45 s at 55 °C and 45 s at 72 °C. Final extension was performed for 5 min at 72 °C. DNA-extractions of *Helicobacter acinonychis* LMG 12684<sup>T</sup> and *Helicobacter mustelae* LMG 8776 were used as positive controls.

#### Analysis of amplified samples

[0090] PCR products were separated on 1 % agarose gels and stained with ethidium bromide.

[0091] DNA-extractions of *H. acinonychis* LMG 12684<sup>T</sup> and *H. mustelae* LMG 8776 were used as positive controls.

[0092] In order to determine whether PCR products were derived from *Helicobacter*-like organisms, the desired DNA-bands were cut from the gels, diluted 1/2 in distilled water and sequenced using the *H33f* and *H1368r* 5'-Indocarbocyanin (Cy5) for "*Candidatus Helicobacter bovis*" and respectively *H61f* and *1492RPL* Indocarbocyanin (Cy5) labeled for "*Candidatus Helicobacter suis*". Partial sequences were screened for homologous sequences using the NCBI GEN-INFO © BLAST Network service (<http://www.ncbi.nlm.nih.gov/BLAST/>) (Altschul et al., 1997).

#### DNA cloning and sequence analysis for "*Candidatus Helicobacter bovis*"

[0093] PCR amplifiers comprising the 16S rDNA-sequences derived from four different stomach samples (R2, R3, R5, R6) were each cloned into plasmid vector pGEM-T (Promega Biotech) according to the manufacturer's instructions and transformed into *Escherichia coli* JM109 using standard procedures. Plasmids were purified using the Easy Prep Plasmid Preparation Kit (Pharmacia Biotech). Sequences were determined by the T7-sequencing system (Pharmacia

Biotech). Two primers flanking the multiple cloning sites (T7, SP6) as well as internal primers *H390f* and *H1053r* were used (Table 2). The sequence derived from the clone of the R2 sample (R2XA) was used as reference sequence. This sequence has been assigned Genbank Accession No. AF127028. Sequence analysis was performed with the PCGene software (Intelligenetics)

[0094] PCR amplicons of three other gastric samples (R13, R27, R28) were sequenced without prior cloning (referred to below as direct sequence analysis).

#### DNA cloning and sequencing for "*Candidatus Helicobacter suis*"

[0095] PCR amplicons comprising the 16S rDNA-sequences from 2 different stomachs (V2B, V4A) were cloned into plasmid vector pGEM-T (Promega Biotech) according to the manufacturer's instructions and transformed into *Escherichia coli* JM109 using standard procedures. Plasmids were purified using the Easy Prep Plasmid Prep Kit (Pharmacia Biotech). Sequences were determined by the T7-sequencing system (Pharmacia Biotech). Two primers flanking the multiple cloning sites (T7 and SP6) as well as internal primers *H390f* and *H1053r* were used (Table 2). Sequence analysis was performed with the PCGene software (Intelligenetics). A reference sequence was determined based on its high length and was compared to the new sequence and the other derived sequences, to check its integrity (see Figures 4 and 5). The reference sequence V2BXA was assigned Genbank Accession No. AF127028.

[0096] PCR amplicons of three other gastric samples (V5, V14, V19) were sequenced without prior cloning (referred to below as direct sequence analysis).

#### Phylogenetic analysis for "*Candidatus Helicobacter bovis*"

[0097] Phylogenetic analysis was performed using the GeneCompass 2.0 software package (Applied Maths). Sequences of strains belonging to the epsilon subdivision (Table 3) were retrieved from the EMBL data library and were aligned with reference sequence R2XA. A similarity matrix was constructed from the aligned sequences and was corrected for multiple base changes by the method of Jukes & Cantor (1969). Unknown bases and gaps were not considered in the numerical analysis. A phylogenetic tree was constructed using the neighbour-joining method of Saitou & Nei (1987).

#### Phylogenetic analysis for "*Candidatus Helicobacter suis*"

[0098] Phylogenetic analysis was performed using the GeneCompass 2.0 software package (Applied Maths). All five "*Candidatus Helicobacter suis*" sequences and the sequences of strains belonging to the same phylogenetic lineage (Table 3) were aligned. Using the neighbour-joining method, a phylogenetic tree and corresponding similarity matrix was constructed. Unknown bases and gaps were not considered in the numerical analysis

#### "*Candidatus Helicobacter bovis*" specific PCR-assay

[0099] "*Candidatus Helicobacter bovis*" specific oligonucleotides *R574f* and *R832r* (Table 2), were selected from variable rDNA regions of the sequences determined by direct and indirect sequence analysis. These primers comprised a 259 bp 16S rDNA-fragment and were used to develop a specific PCR and an *in situ* hybridisation procedure. Within this fragment an internal "*Candidatus Helicobacter bovis*" specific probe *R628f* (Table 2) was selected for southern blot hybridisation purposes.

[0100] PCR reactions were performed in a volume of 50 µl containing 10 mM Tris HCl (pH 8.3), 50 mM KCl, 2.5 mM MgCl<sub>2</sub>, 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold, and 25 pmol of both forward and reverse primer. PCR amplification was performed under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 40 cycles of 30 s at 94 °C, 45 s at 60 °C and 90 s at 72 °C. Final extension was performed for 5 min at 72 °C. All gastric DNA-extracts were tested with this PCR. For positive controls, plasmid DNA was used from the cloned 16S rDNA fragments (R2XA). As a negative control a DNA-extract was used from an abomasum lacking of *Helicobacter-like* organisms.

[0101] Specificity of the "*Candidatus Helicobacter bovis*" specific oligonucleotides *R574f* and *R832r* was tested by PCR using DNA-extracts of 15 different *Helicobacter* strains and a *Wolinella succinogenes* strain (Table 1).

[0102] PCR products were separated on 2 % agarose gels, stained with ethidium bromide and transferred to Hybond N+ (Amersham) by electro-elution. Southern blot hybridisation was performed with the [<sup>32</sup>P] ATP labelled probe *R628f* (Table 2) according to standard procedures (Amersham Pharmacia Biotech). In order to ensure the specificity of the probe hybridisation, blots were washed twice with 0.1 x SSC + 0.1 % SDS at 55°C.

**"*Candidatus Helicobacter suis*" specific diagnostic PCR-assay and Southern blot hybridisation**

[0103] "*Candidatus Helicobacter suis*": specific primers (V832f and V1261r) were selected from variable rDNA regions of the sequences determined by direct and indirect sequence analysis, comprising a ~0.4-Kb 16S rDNA-fragment. Within this fragment a "*Candidatus Helicobacter suis*"-specific probe V1000f (Table 2) was selected for hybridisation purposes. PCR reactions were performed in a volume of 50 µl containing 10 mM Tris HCl (pH 8.3), 50 mM KCl, 2.5 mM MgCl<sub>2</sub>, 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold (Perkin-Elmer), and 25 pmol of both forward and reverse primer (Eurogentec). PCR amplification was performed under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 40 cycles of 30 s at 94 °C, 45 s at 60 °C and 90 s at 72 °C. Final extension was performed for 5 min at 72 °C. As a positive control, plasmid DNA was used from the cloned 16S rDNA fragments (V2B, V4A). As a negative control DNA extracted from the stomach of a gnotobiotic piglet was used.

[0104] To test the specificity of the primers, PCR was also performed on DNA-extracts of 15 different *Helicobacter* species. (Table 1).

[0105] PCR products were separated on 2% agarose gels, stained with ethidium bromide and transferred to Hybond N+ (Amersham) by electro-blotting. Southern blot hybridisation was performed with the [<sup>32</sup>P] ATP-labelled probe V1000f according to standard procedures (Amersham Pharmacia Biotech). In order to ensure the specificity of the probe hybridisation, blots were washed twice with 0.1 x SSC + 0.1 % SDS at 55°C.

***In situ* hybridisation for "*Candidatus Helicobacter bovis*"**

[0106] In order to make the link between the "*Candidatus Helicobacter bovis*" specific probe and the bacterial spiral cells observed in the tissue sections, an *in situ* hybridisation procedure was performed on the formalin fixed and paraffin embedded pyloric samples of each animal. A 259-base digoxigenin-labeled probe was synthesized using the "PCR Dig Probe Synthesis Kit" (Boehringer Mannheim) in combination with the "*Candidatus Helicobacter bovis*" specific primers R574f and R832r (Table 2). PCR conditions were identical to those described in the diagnostic PCR assay. The resulting PCR product was purified using the "High Pure PCR Product Purification Kit" (Boehringer Mannheim) following manufacturer's instructions.

[0107] To avoid RNAse activity, all glassware was heated at 180°C for 3 hours. Further precautions included the use of RNAse-free water, and the use of sterile disposable materials whenever possible. Sections of the paraffin-embedded tissues (4 µm thick) were mounted on RNAse-free, APES-coated slides (Sigma-Aldrich) and fixed by heating for 1 hour at 60 °C. The sections were deparaffinized in xylene (2x5 min), rehydrated through graded ethanol, and washed twice in PBS for 5 min each. Sections were then treated with proteinase K (DAKO) for 15 min each at 37 °C in a humidified chamber. The enzyme was inactivated by treatment with 0.2 % glycine in PBS for 3 min. Sections were washed twice in PBS for 5 min each, dehydrated in graded ethanol and air dried. Tissues were circumcised with a DAKO Pen (DAKO) to avoid liquid spillage during further processing and to ensure an efficient sealing of the coverslip. For the hybridisation step, sections were covered with 5 to 15 µl solution, containing 5 ng/µl labeled probe in 50 % deionized formamide, 2x SSC, 10 % dextran sulfate, 0.25 µg/µl yeast t-RNA, 0.5 µg/µl heat denatured salmon sperm DNA, and 1x Denhart's solution. Sections were covered with a piece of coverslip to avoid evaporation. To denature the probe, sections were heated for 10 min at 95 °C and chilled on ice for 10 min. Slides were then hybridised overnight at 37 °C in a humidified chamber. To remove the unbound probe, the coverslips were removed and the sections were washed in 2x SSC and 1x SSC at room temperature for 10 min each followed by two washes of 0.3x SSC at 40 °C for 10 min and at room temperature for 10 min, respectively.

[0108] All steps involving the immunological detection of the hybridised probe were performed at room temperature. The sections were treated first for 30 minutes in Buffer 1 (100mM Tris HCl, 150 mM NaCl, pH 7.5) containing 2 % normal goat serum and 0.3 % Triton X-100. An incubation step followed for 3 hours with diluted (1:30 in the same solution) anti-digoxigenin antibodies conjugated to horse-radish peroxidase (DAKO). Unbound antibodies were washed gently on a shaker with Buffer 1 followed by Buffer 2 (100 mM Tris HCl, 100 mM NaCl, 50 mM MgCl<sub>2</sub>, pH 9.5) for 15 min each. To optimize the detection level, the "Tyramid Signal Amplification System" (NEN Life Science Products) was applied on each section, following manufacturer's instructions. The hybridised probe was then visualized, using H<sub>2</sub>O<sub>2</sub> with diaminobenzidine as a chromogen (Fast DAB Tablet Set, Sigma-Aldrich). Thereafter the sections were counter-stained with Mayer's hematoxylin and mounted.

***In situ* hybridisation for "*Candidatus Helicobacter suis*"**

[0109] To link the derived sequence to the corresponding organism, an *in situ* hybridisation procedure was performed on the formalin fixed and paraffin embedded pyloric samples of each animal. A ~0.4 Kb digoxigenin-labeled probe was synthesized using the "PCR Dig Probe Synthesis Kit" (Boehringer Mannheim) in combination with the "*Candidatus*

*Helicobacter suis*\*-specific primers V832f and V1261r (Table 2). The rest of the method was performed as mentioned above for "*Candidatus Helicobacter bovis*".

#### Nucleotide sequence accession numbers

[0110] Accession numbers of the 16S rDNA gene sequences used for the phylogenetic analysis are listed in table 3.  
[0111] The 16S rDNA nucleotide sequence of "*Candidatus Helicobacter bovis*" has been deposited in the Genbank database under accession number AF127027.

[0112] The 16S rDNA nucleotide sequence of "*Candidatus Helicobacter suis*" has been deposited in the Genbank database under accession number AF127028.

#### Results

##### Urease activity and immunohistochemical evaluation for the cattle samples

[0113] Urease activity was observed in all pyloric samples (7/7). In the fundic samples, urease activity was absent (0/7). Spiral immunostained organisms were observed in the pyloric samples of all animals. The highest concentration was seen in the most distal pyloric samples. They were mostly situated in the mucus layer and in the lumen of the proximal part of the gastric crypts where they formed small clusters. In some samples, coccoid organisms, were observed between the spiral bacteria, which also crossreacted with the *H. pylori* polyclonal antibodies. In the positive control only *Helicobacter pylori*-like bacteria were stained while in the negative controls no staining was observed.

##### Urease activity and immunohistochemical evaluation for the pig samples

[0114] Tightly coiled immunostained spiral organisms, morphologically similar to "*Gastrospirillum suis*" (Queiroz et al., 1990) were observed in all stomachs (5/5), which was consistent with the presence of urease activity (5/5). The gastrospirillum-like organisms were seen laying separately or in small clusters with a patchy distribution over the sample, and were found mostly in the superficial part of the gastric crypts. Some bacteria revealed bipolar immunostained flagellae. Immunostained coccoid-like organisms were also observed in the pyloric crypts. In the positive control, only *Helicobacter pylori*-like bacteria were stained while in the negative controls no labeling was observed.

##### Transmission electronmicroscopy for "*Candidatus Helicobacter bovis*"

[0115] Large groups of multiple spiral bacteria were seen within the crypts of the gastric mucosa. There was no obvious cell association between the bacteria and the gastric cells, neither were there any intracellular bacterial inclusions. The bacteria were helical-shaped and had 1-3 complete spiral turns per cell with a wavelength of approximately 750 nm. Cells were 1 - 2.5 µm long and 0.3 µm wide. At least four flagelles were seen at one end. It was unclear whether these flagellae were uni- or bipolar, neither could the presence or absence of a flagella sheath be noted.

##### Transmission electronmicroscopy for "*Candidatus Helicobacter suis*"

[0116] Within the gastric crypts of the antral region, longitudinal and transversal sections of spiral organisms could be seen. All bacteria had the same characteristic tightly coiled appearance, typical of *Helicobacters* with the gastrosprillum morphology. The length of cells varied from 2.5 to 3.5 µm and they were approximately 0.6 µm wide. Multiple complete spiral turns with a wavelength of ± 600 nm were seen in all longitudinal sections. As only few longitudinal sections of the bacteria were obtained, the number and implantation of the flagellae could not be studied although partial fragments were observed. The bacteria were not seen intracellularly nor was there any obvious cell association with the surrounding epithelial cells. The presence or absence of a flagella sheath could not be noted.

##### Amplification, cloning and sequencing of *Helicobacter*-like 16S rDNA fragments from cattle samples

[0117] PCR amplification of the 16S rDNA gene using the H33f and H136br primers, produced a fragment of the expected size range (± 1.3 Kbp) in all seven samples examined. Partial direct sequence analysis of four of these bands (R2, R3, R5, R6) and subsequent database comparison (BLAST) confirmed the PCR products to be *Helicobacter*-like 16S rDNA fragments. Four PCR products (R2, R3, R5, R6) were cloned followed by partial screening. In one clone a *Clostridium*-like 16S rDNA fragment was found. In all other clones *Helicobacter*-like fragments were inserted. The 16S rDNA sequences of four clones derived from different animals (R2XA, R3XA, R5XE, R6XA), were determined. Additional sequences of three other samples (R13, R27, R28) were characterized by direct sequence analysis using the

primers H33f, H1368r, H390f and H1053r.

#### Amplification, cloning and sequencing of *Helicobacter*-like 16S rDNA fragments from pig samples

[0118] Several combinations of PCR primers yielded sequences of the expected size. The length of these amplified fragments varied between 1.2 Kb (H274f-1492RPL) and 1.4 Kb (H61f-1492RPL). The latter primer combination was used to examine all samples. The 16S rDNA sequences of two different clones were determined (V2BXA, V4AXA). Additional sequences of 3 other samples (V5, V14, V19) were determined by direct sequence analysis.

#### Sequences and phylogenetic analysis for cattle samples

[0119] Sequence length varied from 1267 to 1335 basepairs. Pairwise comparisons between these 7 sequences revealed a sequence homology of more than 99 %. One reference sequence (R2XA) of 1335 bp (see Figure 1: SEQ ID NO 1) was selected for phylogenetic evaluation. A similarity matrix based on comparisons of 16S rDNA sequences of 23 strains representing all validly named *Helicobacter* species, "*Helicobacter heilmannii*" (type1, type2), *Campylobacter jejuni*, *Arcobacter cryaerophilus* and *Wolinella succinogenes* was calculated. By this analysis it was shown that the sequences of the bovine *Helicobacter*-like organisms form a distinct group within the genus *Helicobacter* with *Helicobacter bilis* as closest taxonomic relative (level of similarity 92.8 %). The reference sequence was clearly distinct from sequences belonging to other superfamily VI genera, as shown by a 85.6, 85.1 % and 89.7 % homology with *Campylobacter jejuni*, *Arcobacter butzleri* and *Wolinella succinogenes* respectively. A phylogenetic tree based on this analysis is shown in Fig. 3A.

#### Sequences and phylogenetic analysis for pig samples

[0120] The 5 sequences that were determined had lengths varying from 1345 to 1421 basepairs. Pairwise comparisons between 1345 bp consensus fragments of these sequences, revealed a minimum homology of 97.7 %. One reference sequence of 1421 bp, obtained from PCR product 2BXA (see Figure 2: SEQ ID NO 2), was used for phylogenetic analysis. A similarity matrix was calculated based on comparisons of 16S rDNA sequences of all *Helicobacter* species, "*Helicobacter heilmannii*" type 1 and type 2, *Campylobacter jejuni*, *Arcobacter butzleri* and *Wolinella succinogenes* (Table 3). In this analysis, the sequence of the porcine gastrospirillum-like organism formed a distinct subgroup within the *Helicobacter* lineage together with other gastrospirilla: *Helicobacter felis*, *H. bizzozeronii*, *H. salomonis*, "*H. heilmannii*" type 1 and type 2. The sequence was highly similar to that of "*H. heilmannii*" type 1 (level of similarity 99.5 %). The similarity level of other gastrospirillum-like bacteria, *H. felis*, *H. bizzozeronii*, *H. salomonis* and *H. heilmannii* type 2 was 96.4 %, 96.5 %, 96.6 % and 96.8 % respectively. The reference sequence was clearly distinct from sequences belonging to other superfamily VI-genera, as shown by a 86.2 %, 84.7 % and 89.6 % homology with *Campylobacter jejuni*, *Arcobacter butzleri* and *Wolinella succinogenes* respectively.

[0121] A phylogenetic tree based on this analysis is shown in Figure 3B.

#### Diagnostic PCR-assay for "*Candidatus Helicobacter bovis*"

[0122] A 259 base fragment was produced for all seven stomach samples with primer pair R574f-R832r. All PCR products crosshybridised with the R628f probe after southern blot hybridisation. No amplification product was obtained using DNA preparations from any of the *Helicobacter* strains, nor from the bovine *Wolinella succinogenes* strain (Table 1). The positive control yielded a ~0.3 Kb product as expected. There was no DNA-amplification using the negative control material.

#### "*Candidatus Helicobacter suis*"-specific PCR and Southern blot hybridisation

[0123] Amplification of *Helicobacter* DNA using the primers V832f and V1261r produced a 433-base fragment from all five stomach samples. All PCR products hybridised with the V1000f probe after Southern blot hybridisation. No amplification product was obtained using DNA preparations from any of the *Helicobacter* strains including *H. felis*, *H. bizzozeronii* and *H. salomonis* (Table 1), nor from the negative control. PCR with the cloned reference material (2BXA) yielded a ~0.4 Kb product as expected.

#### In situ hybridisation for "*Candidatus Helicobacter bovis*"

[0124] In situ hybridisation of the bovine *Helicobacter*-like bacteria with the "*Candidatus Helicobacter bovis*"-specific probe was seen in sections from all (7/7) stomachs. These bacteria were observed as dark brown spiral organisms,

organised in small clusters, situated in the gastric crypts of the pyloric part of the abomasal stomach. Not all spiral bacteria were stained. Sometimes a faint background, seen as fine stained strings, was observed in the surrounding cells. This background staining was also observed in the *H. pylori*-infected mouse stomach which was used as a negative control. The *H. pylori* cells in this control though did not hybridise with the "*Candidatus Helicobacter bovis*"-specific probe.

#### *In situ* hybridisation for "*Candidatus Helicobacter suis*"

[0125] *In situ* hybridisation of "*Gastrospirillum suis*"-like bacteria with the "*Candidatus Helicobacter suis*"-specific probe was seen in sections from all (5/5) stomachs. Bacteria were observed as darkbrown spiral organisms in the superficial mucous layer and the gastric crypts. In some cases, helical organisms located deeply in the crypts, were weakly labeled or were negative. Sometimes a faint background, seen as fine stained strings, was observed in the surrounding cells. This background staining was also observed in the *H. pylori*-infected mouse stomach which was used as a negative control. The *H. pylori* cells in this control though did not hybridise with the "*Candidatus Helicobacter suis*"-specific probe.

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Table 1:

Bacterial strains used for the evaluation of the "Candidatus <i>Helicobacter bovis</i> " specific PCR		
Taxon	Source	Collection N° or Strain
<i>Helicobacter acinonychis</i>	Cheetah gastric mucosa	LMG 12684 <sup>T</sup>
<i>Helicobacter cinaedi</i>	Human feces	LMG 7543 <sup>T</sup>
<i>Helicobacter</i> sp. strain CLO-3	Human rectal swab	LMG 7792
<i>Helicobacter fennelliae</i>	Human feces	LMG 11759
<i>Helicobacter pametensis</i>	Tern feces	LMG 12678 <sup>T</sup>
<i>Helicobacter</i> sp. strain Bird B	Bird feces	LMG 12679
<i>Helicobacter</i> sp. strain Bird C	Bird feces	LMG 13642
<i>Helicobacter hepaticus</i>	Murine liver	LMG 16316 <sup>T</sup>
<i>Helicobacter pullorum</i>	Chicken lower bowel	LMG 16318
<i>Helicobacter mustelae</i>	Ferret gastric mucosa	LMG 18044 <sup>T</sup>
<i>Helicobacter canis</i>	Canine feces	LMG 18086 <sup>T</sup>
<i>Helicobacter muridarum</i>	Murine intestinal mucosa	LMG 14378 <sup>T</sup>
<i>Helicobacter bizzozeronii</i>	Canine gastric mucosa	Strain 12A
<i>Helicobacter salomonis</i>	Canine gastric mucosa	CCUG 37845 <sup>T</sup>
<i>Helicobacter felis</i>	Feline gastric mucosa	CCUG 28539 <sup>T</sup>



Table 2: Oligonucleotide primers and probe used for PCR amplification, sequencing of genes coding for 16S rRNA and Southern blot hybridisation

Primers	Sequences (5'-3')	<i>Escherichia coli</i> 16S rRNA position
<i>H33f</i>	ACG CTG GCG GCG TGC CTA ATA CAT GCA AGT CG	33-64 (SEQ ID NO 3)
<i>H1368r</i>	GGT GAG TAC AAG ACC CGG GAA CGT ATT CAC CG	1368-1388 (SEQ ID NO 4)
<i>H390f</i>	GCA GCA ACG CCG CGT GGA GGA TGA	390-413 (SEQ ID NO 5)
<i>H1053r</i>	ACG AGC TGA CGA CAG CCG TG	1053-1072 (SEQ ID NO 6)
<i>R574f</i>	AGA GCG TGT AGG CGG AAT GAT	574-593 (SEQ ID NO 7)
<i>R628f</i>	AAC TGC GTT TGA AAC TAT CAT T	628-649 (SEQ ID NO 8)
<i>H61f</i>	TGC AAG TCG AAC GAT GAA GC	61-76 (SEQ ID NO 9)
<i>H274f</i>	AGG CTA TGA CGG GTA TCC GGC CTG AGA	274-299 (SEQ ID NO 10)
<i>I492RPL</i>	GCC GCC CGG GTT ACC TTG TTA CGA CTT	832-852 (SEQ ID NO 11)
<i>V832f</i>	TTG GGA GGC TTT GTC TTT CCA	1000-1020 (SEQ ID NO 12)
<i>V1261r</i>	GAT TAG CTC TGC CTC GCG GCT	1261-1281 (SEQ ID NO 13)

V1000f	AGG AAT TCC CTA GAA ATA GGG	1000-1020 (SEQ ID NO 26)
R832r	CGA GGA GAC AAG CCC CCC GA	832-851 (SEQ ID NO 14)

Table 3:

Sources and accession numbers of strains used for phylogenetic analysis.

Taxon	Source	Genbank Accession N°
<i>*Gastrosprillum hominis* type 1</i>	Human gastric mucosa	L10079
<i>*Gastrosprillum hominis* type 2</i>	Human gastric mucosa	L10080
<i>Helicobacter acinonychis</i>	Cheetahgastric mucosa	M88148
<i>Helicobacter bilis</i>	Murine liver	U18766
<i>Helicobacter bizzozeronii</i>	Canine gastric mucosa	Y09404
<i>Helicobacter canis</i>	Canine feces	L13464
<i>Helicobacter cholecystus</i>	Murine liver	U46129
<i>Helicobacter cinaedi</i>	Human feces	M88150
<i>Helicobacter felis</i>	Feline gastric mucosa	M57398
<i>Helicobacter fennelliae</i>	Human feces	M88154
<i>Helicobacter hepaticus</i>	Murine liver	U07574
<i>Helicobacter muridarum</i>	Murine intestinal mucosa	M80205
<i>Helicobacter mustelae</i>	Ferret gastric mucosa	M35048
<i>Helicobacter nemestrinae</i>	Macaque gastric mucosa	X67854
<i>Helicobacter pametensis</i>	Swine feces	M88155
<i>Helicobacter pullorum</i>	Broiler chicken cecum	L36141
<i>Helicobacter pylori</i>	Human gastric mucosa	M88157
<i>Helicobacter salomonis</i>	Canine gastric mucosa	Y09405
<i>Helicobacter trogonum</i>	Rat colon mucosa	U65103
<i>Helicobacter rodentium</i>	Murine intestinal mucosa	U96297
<i>Arcobacter butzleri</i>	Human	L14626
<i>Campylobacter jejuni</i>	Human feces	L14630
<i>Wolinella succinogenes</i>	Cattle abomasal mucosa	M88159

Annex to the application documents - subsequently filed sequences listing

[0185]

## SEQUENCE LISTING

&lt;110&gt; Universiteit Gent

<120> New gastric Helicobacter 16 S rDNA sequences from  
cattle and pigs and their use for detection and typing  
of Helicobacter strains

&lt;130&gt; EP.99.UG.01.DUCA

&lt;140&gt; 99870035.5

&lt;141&gt; 1999-02-25

&lt;160&gt; 25

&lt;170&gt; PatentIn Ver. 2.1

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	cgcaactctaa	gaagactgcc	tgcgtaagca	ggagggaagt	gaggacgacg	tcaagctcat	1080
	atggccctta	cgctaggggc	tacacacgtg	ctacaattgg	gtgcacaaag	agatgcacaa	1140
	ccgcgagcca	gagctaactc	ataaaacacc	tcctagtctg	gattgcaggc	tgcaactcgc	1200
	ctgcatgaag	ctggaatcgc	tagtaatcgc	aaaatcagct	atgttgcggt	gaatacagtc	1260
35	cccgggtctt	gtactcacgc	cccgcgcaca	ccatgggagt	tgtgtttgcc	ttaagctcag	1320
	atgctaaagc	agctactgcc	cacgcacaca	cagcg			1355
	<210> 24						
	<211> 1358						
	<212> DNA						
40	<213> <i>Helicobacter</i> sp.						
	<400> 24						
	agtdghgcac	gggtgagtaa	tgcatagatg	acatgcocct	tagtttggaa	tagccactag	60
	adutgtgtgat	taataccaaa	tactacctta	cgaagggvna	attatcgcta	aaggatttgt	120
45	ctatgtccta	tcagcttgtt	gggtgagtta	aaggctcacc	aagggtctatg	acgggtatcc	180
	ggcctgagag	gktgagcgga	cacactggaa	ctgagacacg	gtccagactc	ctacgggagg	240
	cagcagtagg	gaatatgtgt	caatgggggg	aaacctcgaa	gcagcaacgc	cgctggagg	300
	atgaaggttt	taggatacgka	aactcctttt	gttagagaag	ataatgacgg	tatctaacga	360
	ataaagcccg	gctaactccg	tgccagcagc	cgcgtaata	cggagggtgc	aagcgttact	420
	cggaactcaat	ggcgctaaag	agtgctgtag	cgggaggaca	agtcagggtg	gtgaatccct	480
50	atggcttcaac	catagaaactg	catttbaaac	tatcctctctg	gagtgtggga	gaggttaggtg	540
	gaattctctgg	tgtaggggta	aaatccgtag	agatacaagg	ggatactcat	tgccgaagg	600
	gacctctgtg	aacatcactg	acgctgatgt	cacgaaagcg	tggggagcaa	acaggtattag	660
	ataccctgtgt	agttccacgc	ctaaacgatg	gatgc tagtt	gttggaaggc	tttgtcttcc	720
	cagtaatgca	gctaacgcct	taagcatccc	gcctggggag	tacggtcgca	agattaaaac	780
55	tcaaarggaa	tagacgggga	ccgcacaaag	cgtggagaca	tgtgttttaa	ttcgargwta	840

```

5      cacgaagaac ccttacctag gccttgacat tgaaggaatt cccttagaaa taggggagtg 900
      tctagcttgc tagaccctga aaacaggtgc tgcacggctg tcgtcagctc gtgtcgtgag 960
      atgttggggt aagtcccgca acgagcgcaa ccctttttct tagttgctaa caggttatst 1020
      gcgcactcta agaagactgc ctgcgtaagc aggaggaagg tgaggacgac gtcaagtcat 1080
      catggccctt acgcctaggg ctacacacgt gctacaatgg ggtgcacaaa gagatgcmaa 1140
      gccgcgaggg agagctaata tataaaacac ctcttagttc ggattgcagg ctgcaactcg 1200
10     cctgcataaa gctggaawtc gctagtaaat cgcaaatcca gctatgttgc ggtgaatdmg 1260
      tkccccgggt cttgtactca ccgccccgtc acacccatgg gagttgtgtt tgccttaagt 1320
      caggatgcta aagcagctac tgcccacgca cacacagc          1358

      <210> 25
      <211> 21
      <212> DNA
      <213> Helicobacter sp.

      <400> 25
20     aggaattccc tagaaatagg g                                21

```

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# Claims

1. An isolated 16S rDNA *Helicobacter* polynucleic acid sequence selected from any of the following
  - (a) a sequence represented in any of SEQ ID NO 1 to 2, or, the 16S rRNA sequence encoded thereby,
  - (b) a sequence which hybridizes under stringent conditions to any of the sequences defined in (a).
2. An isolated polynucleic acid sequence according to claim 1 represented by any of SEQ ID NO 1 to 2 or 15 to 24.
3. An isolated polynucleic acid sequence according to claim 1 which is more than 92.8%, preferably more than 93.5%, more preferably more than 95% and most preferably more than 97.5% homologous to SEQ ID NO 1.
4. A part of an isolated polynucleic acid according to any of claims 1 to 3, wherein said part is unique to the polynucleic acid sequence it is derived from.
5. A probe which specifically hybridizes to a polynucleic acid sequence according to any of claims 1 to 4.
6. A primer which specifically amplifies a polynucleic acid sequence according to any of claims 1 to 4.
7. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising hybridizing the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one probe according to claim 5.
8. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically amplifying the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one primer according to claim 6.
9. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically hybridizing or specifically amplifying the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one sequence which is more than 96.6% homologous to SEQ ID NO 2, or a sequence specific primer or a sequence specific probe derived thereof.

10. A diagnostic kit for detection and/or typing of *Helicobacter* strains comprising:

- at least one probe according to claim 5 or 9, and/or,

5       - at least one primer according to claim 6 or 9.

11. A medicament comprising a polynucleic acid sequence according to any of claims 1 to 6.

12. A polynucleic acid sequence according to any of claims 1 to 6 for use as a medicament.

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\*                      20                      \*

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HbovisR2XA : -----ACGCT : 5
Hpylori|gb : TTTATGGAG-----CAGAGTGAACGCT : 37
Hbilis|gb| : -----CAGAGTGAACGCT : 28
Hcanis|gb| : -----CAGAGTGAACGCT : 28
Hcinaedi|g : -TTATGGAG-----CAGAGTGAACGCT : 36
Hacinonych : TTTATGGAG-----CAGAGTGAACGCT : 37
Hnemestrin : NNTATGGAG-----CAGAGTGAACGCT : 37
Hcholescys : -----CAGAGTGAACGCT : 18
Hpamatensi : -TTATGGAG-----CAGAGTGAACGCT : 36
Hmustelael : ATTATGGAG-----CAGAGTGAACGCT : 37
Hrodentium : -----CAGAGTGAACGCT : 14
Hpullorum| : -----G-----CAGAGTGAACGCT : 29
Hfennellia : TTTACGGAG-----CAGAGTGAACGCT : 37
Htrogontum : -----CAGAGTGAACGCT : 14
Hmuridarum : ---ATGGAG-----CAGAGTGAACGCT : 34
Hhepaticus : -----CAGAGTGAACGCT : 13
Ghominis1| : -----AGTGAACGCT : 10
Ghominis2| : -----AGTGAACGCT : 10
Hfelis|gb| : TTTATGGAG-----CAGAGTGAACGCT : 37
Hbizzozero : -----AGTGAACGCT : 10
Hsalomonis : ----- : -
Abutzleri| : ---ATGGAG-----CAGAGTGAACGCT : 34
Cjejunii|gb : --TATGGAG-----CAGAGTGAACGCT : 35
Wsuccinoge : -TTATGGAG-----CAGAGTGAACGCT : 36
cagagtgaacgct

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Figure 1 - 1

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      40          *          60          *
HbovisR2XA : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAA : 42
Hpylori1gb : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hbilis1gb1 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hcanis1gb1 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hcinaedi1g : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 73
Hacinonych : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hnemestrin : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hcholescys : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 55
Hpamatenisi : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 73
Hmustelae1 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hrodentium : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hpullorum1 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 66
Hfennellia : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Htrogonum : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hmuridarum : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 71
Hhepaticus : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 50
Hominis11 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hominis21 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hfelis1gb1 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hbizzozero : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hsalomonis : -----GAAG : 4
Abutzler1 : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 71
Cjejun1gb : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 72
Wsuccinoge : GGC GCG GTGCCTAATACATGCAAGTCGAACGATGAAG : 73
ggcggcggtgcctaatacatgcaagtcgaacgatgag

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Figure 1 - 2

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      80          *          100          *
HbavisR2XA : TTTC-TAGCTTGCCTAGGAATG---GATTAGTGGCGCA : 75
Hpylori1gb : CTTC-TAGCTTGCCTAGGATGCT--GATTAGTGGCGCA : 108
Hbills1gb1 : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 98
Hcanis1gb1 : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 98
Hcinaedi1g : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 106
Hacinonych : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 107
Hnemestrin : CTCT-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 104
Hchoclescys : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 88
Hpamatensi : CTCTCTAGCTTGCCTAGGATG---GATTAGTGGCGCA : 108
Hmustelael : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 107
Hrodentium : C--TCCTAGCTTGCCTAGGATG---GATTAGTGGCGCA : 82
Hpullorum1 : C--TCCTAGCTTGCCTAGGATG---GATTAGTGGCGCA : 99
Hfennellia : TCAC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 107
Htrogonotum : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 84
Hmuridarum : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 104
Hhepaticus : CTTC-TAGCTTGCCTAGGATG---GATTAGTGGCGCA : 83
Ghominis11 : C--C-TAGCTTGCCTAG---TT--GATTAGTGGCGCA : 75
Ghominis21 : C--C-TAGCTTGCCTAG---GTG--GATTAGTGGCGCA : 76
Hfelis1gb1 : C--C-TAGCTTGCCTAG---GCG--GATTAGTGGCGCA : 103
Hbizzozero : C--C-TAGCTTGCCTAG---GTG--GATTAGTGGCGCA : 76
Hsalomonis : C--C-TAGCTTGCCTAG---GCG--GATTAGTGGCGCA : 33
Abutzler1 : GATTATAGCTTGCCTAG---ATTGTCAGCTAGTGGCGCA : 108
Cjejun1gb : C--TCCTAGCTTGCCTAGGATG---GATTAGTGGCGCA : 105
Wsuccinoge : GGCTCTAGCTTGCCTAGCTGCT--GATTAGTGGCGCA : 108
c          TAGCTTGCtag          gattAGTGGCGCA

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Figure 1 \_ 3

	120	*	140	
HbovisR2XA :	CGGGTGAGTAAAGC	ATAG	-AAATGCCCC	TTAGT
Hpylori gb :	CGGGTGAGTAAAGC	ATAG	TCATG	TGCCCTTAGT
Hbilis gb  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hcanis gb  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hcinaedilg :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hacinonych :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hnemestrin :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hcholescys :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hpamateni :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hmustelae  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hrodentium :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hpullorum  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hfennellia :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Htrogontum :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hmuridarum :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hhepaticus :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hgominis1  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hgominis2  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hfelis gb  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hbizzozero :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Hsalomonis :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Habutzeri  :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Cje uni gb :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
Wsuccinoge :	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT
	CGGGTGAGTAAAGC	ATAG	TTAAATGCCC	TTAGT

Figure 1 - 4



		160		180	
HbovisR2XA :	GGGATAGCCAC	CGGAAC	GTGATTAA	TACTAATAC	: 148
Hpylori gb :	GGGATAGCCAT	TGGAAACG	ATGATTAA	TACCAATAC	: 182
Hbilis gb  :	GGGATAGCCAT	TGGAAACGGT	GATTAA	TACTGATAC	: 172
Hcanis gb  :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACTGATAC	: 172
Hcinaedilg :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACTGATAC	: 180
Hacinonych :	GGGATAGCCAT	TGGAAACGGT	GATTAA	TACCAATAT	: 181
Hnemestrin :	GGGATAGCCAT	TGGAAACG	ATAGATAA	TACCAATAC	: 178
Hcholescys :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACTCGATAC	: 162
Hpmatensi :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACTAATAC	: 182
Hmustelae  :	GGGATAGCCAT	TGGAAACGGT	GATTAA	TACTGATAC	: 181
Hrodentium :	GGGATAGCCAT	TGGAAACG	ATGATTAA	TACTGATAC	: 156
Hpullorum  :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACTAATAC	: 173
Hfennellia :	GGGATAHNNN	TNGAAACGGT	GATTAA	TACNNNNNN	: 181
Htrogontum :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACCGATAC	: 158
Hmuridarum :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACTGATAC	: 178
Hhepaticus :	GGGATAGCCA	TGGAAACGGT	GATTAA	TACTGATAC	: 157
Ghominis1  :	GGGATAGCCAT	TAGAAATGGT	GATTAA	TACCAATAC	: 149
Ghominis2  :	GGGATAGCCAT	TAGAAATGGT	GATTAA	TACCAATAT	: 150
Hfelis gb  :	GGGATAGCCAT	TAGAAATGGT	GATTAA	TACCAATAC	: 177
Hbizzozero :	GGGATAGCCAT	TAGAAATGGT	GATTAA	TACCAATAC	: 150
Hsalomonis :	GGGATAGCCAT	TAGAAATGGT	GATTAA	TACCAATAC	: 107
Abutzler  :	GGGATAGCCAT	TGGAAACG	ATGCAATAC	CTTATAT	: 182
Cjejun gb :	AGGACACAGT	TGGAAACG	ACTGCTNA	TACTCTATAC	: 179
Wsuccinoge :	GGGATAGCCAT	TGGAAACGGT	GATTAA	TACCGATAT	: 182
	GgGAtAgCca	tgGAAACggtgat	TAATAC	ATAC	

Figure 1-5

	*	200	*	220	
HbavisR2XA :	G	C	C	T	-----AAGGGGGAAGCA--ATT : 169
Hpylori gb :	T	-	C	C	T-----AAGGGGGAAGCA--TTT : 201
Hbilis gb  :	T	C	C	C	T-----AAGGGGGAAGCA--TTT : 195
Hcanis gb  :	T	C	C	C	T-----AAGGGGGAAGCA--TTT : 191
Hcinaedi g :	T	C	C	T	-----AAGGGGGAAGCA--TTT : 199
Hacinonych :	T	-	C	C	T-----AAGGGGGAAGCA--TTT : 200
Hnemestrin :	T	-	C	C	T-----AAGGGGGAAGCA--TTT : 197
Hcholescys :	T	-	C	C	C-----TACGGGGAAGCA--TTT : 181
Hpmatensi :	T	-	C	C	T-----TACGGGGAAGCA--TTT : 201
Hmustelae  :	T	-	C	C	T-----AAGGGGGAAGCA--TTT : 200
Hrodentium :	T	C	C	C	T-----AAGGGGGAAGCA--TTT : 175
Hpullorum  :	T	C	C	C	T-----AAGGGGGAAGCA--TTT : 192
Hfennellia :	M	-	M	N	N-----MNNH.MNNMNN--MNC : 200
Htrogontum :	T	C	C	T	T-----AAGGGGGAAGCA--TTT : 177
Hmuridarum :	T	C	C	T	-----T-----AAGGGGGAAGCA--TTT : 196
Hhepaticus :	T	C	C	C	T-----AAGGGGGAAGCA--TTT : 176
Ghominis1  :	T	A	C	C	T-----AAGGGGGAAGCA--TTT : 170
Ghominis2  :	T	A	C	C	T-----AAGGGGGAAGCA--TTT : 171
Hfelis gb  :	T	-	C	C	T-----AAGGGGGAAGCA--TTT : 196
Hbizzozero :	T	A	C	C	T-----AAGGGGGAAGCA--TTT : 171
Hsalomonis :	T	A	C	C	T-----AAGGGGGAAGCA--TTT : 128
Abutzerli  :	T	C	T	T	T T T T T A T C A A A A G A T A A A A G G G A A A C A --TTT : 216
Cjejunilgb :	T	C	T	T	G C T T A A C A A A G T T G T A G A A A A G --TTT : 212
Wsuccinoge :	T	C	C	C	T-----AAGGGGGAAGCA--TTT : 201
	t	c		a	gggGGAAG TTT

Figure 1 - 6

	*	240	*	26	
HbovisR2XA :	-----				:
Hpylori gb :	-----				:
Hbilis gb  :	CAATAAAGAATTTCTCTTTTAGTGCTTTGTGTTGTT	:			232
Hcanis gb  :	-----				:
Hcinaedi g :	-----				:
Hacinonych :	-----				:
Hnemestrin :	-----				:
Hcholescys :	-----				:
Hpamatensi :	-----				:
Hmustelae  :	-----				:
Hrodentium :	-----				:
Hpullorum  :	-----				:
Hfennellia :	-----				:
Htrogontum :	-----				:
Hmuridarum :	-----				:
Hhepaticus :	-----				:
Ghominis1  :	-----				:
Ghominis2  :	-----				:
Hfelis gb  :	-----				:
Hbizzozero :	-----				:
Hsalomonis :	-----				:
Abutzleri  :	-----				:
Cjejuni gb :	-----				:
Wsuccinoge :	-----				:

Figure 1 - 7

	0	*	280	*	
HbovisR2XA :	-----	-----	-----	-----	-
Hpylori gb :	-----	-----	-----	-----	-
Hbilis gb  :	GGCACAAAATTCTAGTATTGGAATGAGAAATTGATG :				269
Hcanis gb  :	-----	-----	-----	-----	-
Hcinaedi g :	-----	-----	-----	-----	-
Hacinonych :	-----	-----	-----	-----	-
Hnemestrin :	-----	-----	-----	-----	-
Hcholescys :	-----	-----	-----	-----	-
Hpamatensi :	-----	-----	-----	-----	-
Hmustelae  :	-----	-----	-----	-----	-
Hrodentium :	-----	-----	-----	-----	-
Hpullorum  :	-----	-----	-----	-----	-
Hfennellia :	-----	-----	-----	-----	-
Htrogontum :	-----	-----	-----	-----	-
Hmuridarum :	-----	-----	-----	-----	-
Hhepaticus :	-----	-----	-----	-----	-
Ghominis1  :	-----	-----	-----	-----	-
Ghominis2  :	-----	-----	-----	-----	-
Hfelis gb  :	-----	-----	-----	-----	-
Hbizzozero :	-----	-----	-----	-----	-
Hsalomonis :	-----	-----	-----	-----	-
Abutzleri  :	-----	-----	-----	-----	-
Cjejunilgb :	-----	-----	-----	-----	-
Wsuccinoge :	-----	-----	-----	-----	-

Figure 1 - 8

	300	*	320	*	
HbovisR2XA :	-----		-----		-
Hpylori gb :	-----		-----		-
Hbilis gb  :	TTGTGAAGCAATT		TGTGCGGAGACTAGACTTAGTGTC		306
Hcanis gb  :	-----		-----		-
Hcinaedi g :	-----		-----		-
Hacinonych :	-----		-----		-
Hnemestrin :	-----		-----		-
Hcholescys :	-----		-----		-
Hpamatensi :	-----		-----		-
Hmustelae  :	-----		-----		-
Hrodentium :	-----		-----		-
Hpullorum  :	-----		-----		-
Hfennellia :	-----		-----		-
Htrogontum :	-----		-----		-
Hmuridarum :	-----		-----		-
Hhepaticus :	-----		-----		-
Ghominis1  :	-----		-----		-
Ghominis2  :	-----		-----		-
Hfelis gb  :	-----		-----		-
Hbizzozero :	-----		-----		-
Hsalomonis :	-----		-----		-
Abutzleri  :	-----		-----		-
Cjejun gb :	-----		-----		-
Wsuccinoge :	-----		-----		-

Figure 1 - 9

	340	*	360	*	
HbovisR2XA :	-----	-----	-----	-----	-
HpyloriIgb :	-----	-----	-----	-----	-
HbilisIgbI :	TGTCGCACAAGCAAAT	TGCGAACTCATCGATT	TATCG		343
HcanisIgbI :	-----	-----	-----	-----	-
HcinaediIg :	-----	-----	-----	-----	-
Hacinonych :	-----	-----	-----	-----	-
Hnemestrin :	-----	-----	-----	-----	-
Hcholescys :	-----	-----	-----	-----	-
Hpamatensi :	-----	-----	-----	-----	-
HmustelaeI :	-----	-----	-----	-----	-
Hrodentium :	-----	-----	-----	-----	-
HpullorumI :	-----	-----	-----	-----	-
Hfennellia :	-----	-----	-----	-----	-
Htrogontum :	-----	-----	-----	-----	-
Hmuridarum :	-----	-----	-----	-----	-
Hhepaticus :	-----	-----	-----	-----	-
Ghominis1I :	-----	-----	-----	-----	-
Ghominis2I :	-----	-----	-----	-----	-
HfelisIgbI :	-----	-----	-----	-----	-
Hbizzozero :	-----	-----	-----	-----	-
Hsalomonis :	-----	-----	-----	-----	-
AbutzlerI :	-----	-----	-----	-----	-
Cjejunilgb :	-----	-----	-----	-----	-
Wsuccinoge :	-----	-----	-----	-----	-

Figure 1 - 10

	380	*	400	
HbovisR2XA :	-----	-----	CGCTAAG :	176
Hpylori gb :	-----	AT-----	CGCTAAG :	210
Hbilis gb  :	TCCAAAGACGAATTTTATTGAAAGCCTT	-----	CGCTAAG :	380
Hcanis gb  :	-----	T-----	CGCTAAG :	200
Hcinaedi g :	-----	T-----	CGCTAAG :	208
Hacinonych :	-----	AT-----	CGCTAAG :	209
Hnemestrin :	-----	AT-----	CGCTAAG :	206
Hcholescys :	-----	TT-----	CGCTAAG :	190
Hpamatensi :	-----	TT-----	CGCTAAG :	210
Hmustelae  :	-----	TT-----	CGCTAAG :	209
Hrodentium :	-----	TT-----	CGCTAAG :	184
Hpullorum  :	-----	TT-----	CGCTAAG :	201
Hfennellia :	-----	TC-----	CGCTAAG :	209
Htrogontum :	-----	TT-----	CGCTAAG :	186
Hmuridarum :	-----	TT-----	CGCTAAG :	205
Hhepaticus :	-----	TT-----	CGCTAAG :	185
Ghominis1  :	-----	AT-----	CGCTAAG :	179
Ghominis2  :	-----	AT-----	CGCTAAG :	180
Hfelis gb  :	-----	AT-----	CGCTAAG :	205
Hbizzozero :	-----	AT-----	CGCTAAG :	180
Hsalomonis :	-----	AT-----	CGCTAAG :	137
Habutzleri  :	-----	NT-----	CGCTAAG :	225
Cjejunilgb :	-----	TT-----	CGCTAAG :	221
Wsuccinoge :	-----	TT-----	CGCTAAG :	210
		t	cGcTa	

Figure 1 - II

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      *           420           *           440
HbovisR2XA : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 213
Hpylori|gb : AGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 247
Hbilis|gb| : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 417
Hcanis|gb| : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 237
Hcinaedilg : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 245
Hacinonych : AGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 246
Hnemestrin : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 243
Hcholescys : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 227
Hpamateni : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 247
Hmustelael : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 246
Hrodentium : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 221
Hpullorum| : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 238
Hfennellia : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 246
Htrogontum : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 223
Hmuridarum : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 242
Hhepaticus : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 222
Ghominis1| : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 216
Ghominis2| : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 217
Hfelis|gb| : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 242
Hbizzozero : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 217
Hsalomonis : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 174
Abutzleril : AGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 262
Cjejunilgb : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 258
Wsuccinoge : GGATGAGCTATGTCCTATCAGCTTGGTGAGGTA : 247
gGAT G CTAgtccTATCAGCTtGTTGGTgaGGA

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Figure 1 - 12



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      *               460               *               480
HbovisR2XA : AATGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 250
Hpylori1gb : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 284
Hpylori1gb : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 284
Hbilis1gb1 : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 454
Hcanis1gb1 : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 274
Hcinaedi1g : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 282
Hacinonych : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 283
Hnemestrin : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 280
Hcholescys : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 264
Hpmatensi : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 284
Hmustelael : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 283
Hrodentium : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 258
Hpullorum1 : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 275
Hfennellia : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 283
Htrogontum : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 260
Hmuridarum : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 279
Hhepaticus : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 259
Ghominis11 : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 253
Ghominis21 : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 254
Hfelis1gb1 : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 279
Hbizzozero : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 254
Hsalomonis : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 211
Abutzler1 : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 299
Cjejunilgb : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 295
Wsuccinoge : AAGGCTTACCAAGGCTATGACGGGTATCCGGCCTGAG : 284
A gGCT ACCAAGGCTATGACGGGTATCCGGCCTGAG

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Figure 1 - 13

\*                      500                      \*

HbovisR2XA : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 287  
Hpylori|gb : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 321  
Hbills|gb| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 491  
Hcanis|gb| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 311  
Hcinaedil|g : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 319  
Hacinonych : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 320  
Hnemestrin : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 317  
Hcholescys : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 301  
Hpmatensi : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 321  
Hmustelae| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 320  
Hrodentium : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 295  
Hpullorum| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 312  
Hfennellia : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 320  
Htrogontum : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 297  
Hmuridarum : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 316  
Hhepaticus : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 296  
Ghominis1| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 290  
Ghominis2| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 291  
Hfelis|gb| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 316  
Hbizzozero : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 291  
Hsalomonis : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 248  
Abutzler| : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 336  
Cjejun|gb : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 332  
Wsuccinoge : AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG : 321  
AGGGTGAATCGGACACACTGGAACTGAGACACGGTCCG

Figure 1 - 14

	20	*	540	*	
HbovisR2XA :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	324	
HpyloriIgb :	GACTCCTAAGGAGGAGGCAGT	AGGGAATATTGCTCA	:	358	
HbillsIgbI :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	528	
HcanisIgbI :	GACTCCTAAGGAGGAGGCAGT	AGGGAATATTGCTCA	:	348	
HcinaediIg :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	356	
Hacinonych :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	357	
Hnemestrin :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	354	
Hcholescys :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	338	
Hpamatensi :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	358	
HmustelaeI :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	357	
Hrodentium :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	332	
HpullorumI :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	349	
Hfennellia :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	357	
Htrogontum :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	334	
Hmuridarum :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	353	
Hhepaticus :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	333	
Ghominis1I :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	327	
Ghominis2I :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	328	
HfelisIgbI :	GACTCCNCGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	353	
Hbizozero :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	328	
Hsalomonis :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	285	
AbutzleriI :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	373	
CjejunIgb :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	369	
Wsuccinoge :	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	358	
	GACTCCTACGGGAGGCAGCAGT				

Figure 1 - 15

	560	*	580	*	
HbovisR2XA :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 361
Hpylori gb :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 395
Hbills gb  :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 565
Hcanis gb  :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 385
Hcinaedi g :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 393
Hacinonych :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 394
Hnemestrin :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 391
Hcholescys :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 375
Hpmatensi :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 395
Hmustelael :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 394
Hrodentium :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 369
Hpullorum  :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 386
Hfennellia :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 394
Htrogontum :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 371
Hmuridarum :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 390
Hhepaticus :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 370
Ghominis1  :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 364
Ghominis2  :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 365
Hfelis gb  :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 390
Hbizzozero :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 365
Hsalomonis :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 322
Abutzler  :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 410
Cjejun gb :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 406
Wsuccinoge :	ATGGGGGAAAC	CC	TGAAGCAGCAACGCCG	GTGGAGG	: 395
	ATGGg	GaAA	ccTGAaGCAGCAACGCCG	GTGGAGG	

Figure 1 - 16

	600	*	620	
HbovisR2XA :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 398
Hpylori gb :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 432
Hbills gb  :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 602
Hcanis gb  :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 422
Hcinaedi g :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 430
Hacinonych :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 431
Hnemestrin :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 428
Hcholescys :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 412
Hpamateni :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 432
Hmustelae  :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 431
Hrodentium :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 406
Hpullorum  :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 423
Hfennellia :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 431
Htrogontum :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 408
Hmuridarum :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 427
Hhepaticus :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 407
Ghominis1  :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 401
Ghominis2  :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 402
Hfelis gb  :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 427
Hbizzozero :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 402
Hsalomonis :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 359
Abutzeri  :	ATGACACATT	TGGTGGCTAAACTCCTTTT	ATATAG	: 447
Cjejunilgb :	ATGACACATT	TGGTGGCTAAACTCCTTTT	ATAGGG	: 443
Wsuccinoge :	ATGAAGGTTT	TAGGATTGTAACTCCTTTT	TCAGAG	: 432
	ATGAaggttttAgGattGTAAACTCCTTTT T agag			

Figure 1 - 17

		640		660	
HbevisR2XA :	AAGG	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 434
Hpylori gb :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 468
Hbilis gb  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 638
Hcanis gb  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 458
Hcinaedilg :	AAGG	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 466
Hacinonych :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 467
Hnemestrin :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 464
Hcholescys :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 448
Hpmatensi :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 468
Hmustelae  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 467
Hrodentium :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 442
Hpullorum  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 459
Hfennellia :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 467
Htrogontum :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 444
Hmuridarum :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 463
Hhepaticus :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 443
Ghominis1  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 437
Ghominis2  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 438
Hfelis gb  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 463
Hbizzozero :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 437
Hsalomonis :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 395
Abutzler1  :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 483
Cjejunigb :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 480
Wsuccinoge :	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	: 468
	AAGA	TATGACGGTATCTT	AG	GAATAAGCACCGGCT	

Figure 1 - 18

	*	680	*	700	
HbovisR2XA :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	471	
Hpylori gb :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	505	
Hbilis gb  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	675	
Hcanis gb  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	495	
Hcinaedi g :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	503	
Hacinonych :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	504	
Hnemestrin :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	501	
Hcholescys :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	485	
Hpmatensi :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	505	
Hmustelae  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	504	
Hrodentium :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	479	
Hpullorum  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	496	
Hfennellia :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	504	
Htrogontum :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	481	
Hmuridarum :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	500	
Hhepaticus :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	464	
Ghominis1  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	474	
Ghominis2  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	475	
Hfelis gb  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	500	
Hbizzozero :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	474	
Hsalomonis :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	432	
Abutzleri  :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	520	
Cjejunii gb :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	517	
Wsuccinoge :	AACTCCGTGCCAGCAGCCGCGGT	AATACGGAGGGTGC	:	505	

Figure 1 - 19

	*	720	*	740	
HbovisR2XA :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				508
Hpylori1gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				542
Hbilis1gb1 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				712
Hcanis1gb1 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				532
Hcinaedi1g :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				540
Hacinonych :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				541
Hnemestrin :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				538
Hcholescys :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				522
Hpamatensi :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				542
Hmustelael :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				541
Hrodentium :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				516
Hpullorum1 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				533
Hfennellia :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				541
Htrogontum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				518
Hmuridarum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				537
Hhepaticus :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				501
Ghominis11 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				511
Ghominis21 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				512
Hfelis1gb1 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				537
Hbizzozero :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				511
Hsalomonis :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				469
Abutzleril :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				557
Cjejunilgb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				554
Wsuccinoge :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGT				542

Figure 1 - 20



760

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HbovisR2XA : AGGCGGAAATGAAAGTCAGGCTGTGAAATCCCGTAGCT : 545
Hpylori|gb : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 579
Hbilis|gb| : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 749
Hcanis|gb| : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 569
Hcinaedilg : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 577
Hacinonych : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 578
Hnemestrin : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 575
Hcholescys : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 559
Hpmatensi : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 579
Hmustelael : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 578
Hrodentium : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 553
Hpullorum| : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 570
Hfennellia : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 578
Htrogontum : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 555
Hmuridarum : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 574
Hhepaticus : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 538
Ghominis1| : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 548
Ghominis2| : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 549
Hfelis|gb| : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 574
Hbizzozero : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 548
Hsalomonis : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 506
Abutzler1| : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 594
Cjejun1|gb : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 591
Wsuccinoge : AGGCGGGAATGAAAGTCAGCTGTGAAATCCTTTAGCT : 579
AGGCGGg t aAGTcag tGTGAAATCct t GCT

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Figure 1 - 21

	780	*	800	*
HbovisR2XA :	TAAC TGGGGAAGTGGGTTGAAACTTCCTCTGGAG :			582
Hpylori gb :	TAAGCAAGAGACTGCATTGAAACTTCTCTGGAG :			616
Hbilis gb  :	TAAC TCGAGAACTGCA TTGAAACTTCTCTGGAG :			786
Hcanis gb  :	TAAC TCGAGAACTGCA TTGAAACTTCTCTGGAG :			606
Hcinaedilg :	TAAC TCGAGAACTGCA TTGAAACTGACTATCTGGAG :			614
Hacinonych :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			615
Hnemestrin :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			612
Hcholescys :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			596
Hpmatensi :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			616
Hmustelael :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			615
Hrodentium :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			590
Hpullorum  :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			607
Hfennellia :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			615
Htrogontum :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			592
Hmuridarum :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			611
Hhepaticus :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			575
Ghominis1  :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			585
Ghominis2  :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			586
Hfelis gb  :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			611
Hbizzozero :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			585
Hsalomonis :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			543
Abutzleri  :	TAAC TCGAGAACTGCATTGAAACTTCTCTGGAG :			631
Cjejun gb :	TAAC TCGTAAACTGCTTGGAAACTGAGTCTCTGGAG :			628
Wsuccinoge :	TAAC TCGTAAACTGCA TTGAAACTGAGGCTCTGGAG :			616
	TAAC a agAACTGC a TtgAACT a tCT Gag			

Figure 1 - 22

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      820          *          840          *
HbovisR2XA : TTTGGGAGAGGTCAGGTGGAACTCTTGGGTAGGGGTA : 619
Hpylori|gb : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 653
Hbilis|gb| : CATGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 823
Hcanis|gb| : CATGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 643
Hcinaedi|g : CATGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 651
Hacinonych : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 652
Hnemestrin : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 649
Hcholescys : CATGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 633
Hpamatensi : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 653
Hmustelael : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 652
Hrodentium : CATGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 627
Hpullorum| : CATGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 644
Hfennellia : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 652
Htrogontum : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 629
Hmuridarum : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 648
Hhepaticus : CATGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 612
Ghominis1| : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 622
Ghominis2| : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 623
Hfelis|gb| : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 648
Hbizzozero : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 622
Hsalomonis : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 580
Abützleri| : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 668
Cjejun|gb : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 665
Wsuccinoge : TTTGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA : 653
T LGGGAGAGGTAAGTGGAAATCTTGGGTAGGGGTA

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Figure 1 - 23

	860	*	880	
HbovisR2XA :	AAATCCGTAGAGATCAAGATCAATCTCATTGCCGAAG			: 656
Hpylori gb :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 690
Hbllis gb  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 860
Hcanis gb  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 680
Hcinaedi g :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 688
Hacinonych :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 689
Hnemestrin :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 686
Hcholescys :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 670
Hpmatensi :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 690
Hmustelae  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 689
Hrodentium :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 664
Hpullorum  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 681
Hfennellia :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 689
Htrogontum :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 666
Hmuridarum :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 685
Hhepaticus :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 649
Ghominis1  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 659
Ghominis2  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 660
Hfelis gb  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 685
Hbizzozero :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 659
Hsalomonis :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 617
Abutzleri  :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 705
Cjejunigb :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 702
Wsuccinoge :	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			: 690
	AAATCCGTAGAGATCAAGAGGGAATCTCATTGCCGAAG			

Figure 1 - 24

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          *           900           *           920
HbovisR2XA : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 692
Hpylori|gb : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 727
Hbills|gb| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 896
Hcanis|gb| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 716
Hcinaedi|g : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 724
Hacinonych : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 726
Hnemestrin : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 723
Hcholescys : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 706
Hpmatensi : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 726
Hmustelae| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 725
Hrodentium : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 700
Hpullorum| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 717
Hfennellia : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 725
Htrogontum : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 702
Hmuridarum : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 721
Hhepaticus : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 685
Ghominis1| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 696
Ghominis2| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 697
Hfelis|gb| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 721
Hbizzozero : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 696
Hsalomonis : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 654
Abutzler| : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 741
Cjejun|gb : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 738
Wsuccinoge : GCGACCTGCTGGAACA tACTGACGCTGAT GCACGA : 726
GCGACCTGCTGGAACA tACTGACGCTGAT gc CgA

```

Figure 1 - 25

		*	940	*	960	
HbovisR2XA :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					729
HpyloriIgb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					764
HbillsIgbI :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					933
HcanisIgbI :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					752
HcinaediIgb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					761
Hacinonych :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					763
Hnemestrin :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					760
Hcholescys :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					743
Hpamatensi :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					763
HmustelaeI :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					762
Hrodentium :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					737
HpullorumI :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					753
Hfennellia :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					762
Htrogontum :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					739
Hmuridarum :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					758
Hhepaticus :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					722
Ghominis1I :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					733
Ghominis2I :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					734
HfelisIgbI :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					758
Hbizzozero :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					733
Hsalomonis :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					691
Abutzlerii :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					778
CjejunIgb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					775
Wsuccinoge :	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG :					763
	AAGCGTGGGGAGCAAACAGGATTAGATACCCCTGGTAG					

Figure 1 - 26

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          *          980          *          100
HbovisR2XA : TCCACGCCCTAAACGATGCTGCTAATTGCGGGGG : 766
Hpylori1gb : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGAGGG : 801
Hbills1gb1 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTG : 970
Hcanis1gb1 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTG : 789
Hcinaedi1g : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTG : 798
Hacinonych : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGG : 800
Hnemestrin : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGAGGG : 797
Hcholescys : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGTG : 780
Hpmatensi : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGAG : 800
Hmustelae1 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGTG : 799
Hrodentium : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGAGG : 774
Hpullorum1 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGAGG : 790
Hfennellia : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTG : 799
Htrogontum : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTG : 776
Hmuridarum : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTTG : 795
Hhepaticus : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTTG : 759
Hhominis11 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGG-AGG : 769
Hhominis21 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGG : 771
Hfelis1gb1 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGG : 795
Hbizzozero : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGG : 770
Hsalomonis : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGG : 728
Habutzer11 : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGAGG : 815
Hcjun11gb : TCCACGCCCTAAACGATGCTGCTAGTTGTTGGGGT : 812
Hsuccinoge : TCCACGCCCTAAACGATGCTGCTAGTTGTTGCCCTG : 800
TCCACGCCCTAAACGATG AtGCTAgTTGTG G

```

Figure 1 - 27

	0	*	1020	*	
HbovisR2XA :	CTT	GTCTCCT	GGTAATGCAGCTAACGC	TTAAGCA	: 802
Hpylori gb :	CTT	AGTCTCTC	CAGTAATGCAGCTAACGC	TTAAGCA	: 838
Hbilis gb  :	CTT	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 1006
Hcanis gb  :	CTT	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 825
Hcinaedi g :	CTT	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 834
Hacinonych :	CTT	GTGYYYC	CAGTAATGCAGCTAACGC	TTAAGCA	: 837
Hnemestrin :	CTT	ATCTCTC	CAGTAATGCAGCTAACGC	TTAAGCA	: 834
Hcholescys :	CTT	GTGACTC	CAGTAATGCAGCTAACGC	TTAAGCA	: 816
Hpmatensi :	CTT	GTCTCTC	CAGTAATGCAGCTAACGC	TTAAGCA	: 836
Hmustelae  :	CTT	GTGACTC	CAGTAATGCAGCTAACGC	TTAAGCA	: 835
Hrodentium :	CTT	GTGCTTG	CAGTAATGCAGCTAACGC	TTAAGCA	: 810
Hpullorum  :	CTT	GTGCTTG	CAGTAATGCAGCTAACGC	TTAAGCA	: 826
Hfennellia :	CTC	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 835
Htrogontum :	CTT	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 812
Hmuridarum :	CTT	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 831
Hhepaticus :	CTT	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 795
Ghominis1  :	CTT	GTCTTTG	CAGTAATGCAGCTAACGC	TTAAGCA	: 806
Ghominis2  :	CTT	GTCTCTC	CAGTAATGCAGCTAACGC	TTAAGCA	: 808
Hfelis gb  :	CTT	GTCTCTC	CAGTAATGCAGCTAACGC	TTAAGCA	: 831
Hblizzozero :	CTT	GTGCCCC	CAGTAATGCAGCTAACGC	TTAAGCA	: 807
Hsalomonis :	CTT	GTGCCCC	CAGTAATGCAGCTAACGC	TTAAGCA	: 765
Abutzleri  :	CTC	GTGCTTG	CAGTAATGCAGCTAACGC	TTAAGCA	: 851
Cjejunilgb :	CTA	GTGCTTG	CAGTAATGCAGCTAACGC	TTAAGCA	: 848
Wsuccinoge :	CTT	GTGAGGG	CAGTAATGCAGCTAACGC	TTAAGCA	: 836
	Ctt	Gtc	CaGTAATGCAGCTAACGC	TTAAGCA	

Figure 1 - 28



	1040	*	1060	*	
HbovisR2XA :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				839
Hpylori1gb :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				875
Hbilis1gb1 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				1043
Hcanis1gb1 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				862
Hcinaedi1g :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				871
Hacinonych :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				874
Hnemestrin :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				871
Hcholescys :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				853
Hpamatensi :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				873
Hmustelae1 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				872
Hrodentium :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				847
Hpullorum1 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				863
Hfennellia :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				872
Htrogontum :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				849
Hmuridarum :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				868
Hhepaticus :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				832
Chominis1 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				842
Ghominis21 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				845
Hfelis1gb1 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				868
Hbizzozero :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				844
Hsalomonis :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				802
Abutzler1 :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				888
Cjejun1gb :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				885
Wsuccinoge :	TTCCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				873
	T CCGCCTGGGGAGTACGGTCCGAAGATTAAACTCA				

Figure 1 - 29

	1080	*	1100	*	
HbovisR2XA :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 876
Hpylori gb :	AAGGAATAAGCGGGACCGCACAAGCGGTGGAGCAT				: 912
Hbillis gb  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 1080
Hcanis gb  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 899
Hcinaedi g :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 908
Hacinonych :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 911
Hnemestrin :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 908
Hcholescys :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 890
Hpmatensi :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 910
Hmustelae  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 909
Hrodentium :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 884
Hpullorum  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 900
Hfennellia :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 909
Htrogontum :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 886
Hmuridarum :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 905
Hhepaticus :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 869
Ghominis1  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 878
Ghominis2  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 882
Hfelis gb  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 905
Hbizzozero :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 881
Hsalomonis :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 839
Abutzleri  :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 925
Cjejunilgb :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 922
Wsuccinoge :	AAGGAATAGACGGGGACCGCACAAGCGGTGGAGCAT				: 910

Figure 1 - 30

	1120	*	1140	
HbovisR2XA :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 913
Hpylori1gb :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 949
Hbills1gb1 :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 1117
Hcanis1gb1 :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 936
Hcinaedilg :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 945
Hacinonych :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 948
Hnemestrin :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 945
Hcholescys :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 927
Hpmatensi :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 947
Hmustelael :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 946
Hrodentium :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 921
Hpullorum1 :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 937
Hfennellia :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 946
Htrogontum :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 923
Hmuridarum :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 942
Hhepaticus :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 906
Ghominis11 :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 915
Ghominis21 :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 919
Hfelis1gb1 :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 942
Hbizzozero :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 918
Hsalomonis :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 876
Habut2ler1 :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 962
Cjejun1gb :	GTGGTTTAATT	CGAAGATAC	CGAAGAACCCTTACCTA	: 959
Wsuccinoge :	GTGGTTTAATT	CGAANNHAC	CGAAGAACCCTTACCTA	: 947
	GTGGTTTAATT	CGAAGA	CGAAGAACCCTTACCTA	

Figure 1 - 31

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      *           1160           *           1180
HbovisR2XA : GGCTTGACATTGAGAGGAATCCATCCCAAGCTGGAG : 950
Hpylori|gb : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 986
Hbilis|gb| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 1154
Hcanis|gb| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 973
Hcinaedi|g : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 982
Hacinonych : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 985
Hnemestrin : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 982
Hcholescys : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 964
Hpmatensi : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 984
Hmustelae| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 983
Hrodentium : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 958
Hpullorum| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 974
Hfennellia : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 983
Htrogonum : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 960
Hmuridarum : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 979
Hhepaticus : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 943
Hghominis1| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 952
Hghominis2| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 956
Hfelis|gb| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 979
Hbizzozero : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 955
Hsalomonis : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 913
Habutzeri| : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 999
Cjejuni|gb : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 996
Wsuccinoge : GGCTTGACATTGAGAGGAATCCCTAGAAATAGTGGAG : 984
GgCTTGACAttga aGAATc ctagA Atag ggaG

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Figure 1 - 32

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      *           1200           *           1220
HbovisR2XA : TGCACGTTTCCTGGAGCTGAAACAGGTGCTGCAC : 986
Hpylori|gb : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1023
Hbills|gb| : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1190
Hcanis|gb| : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1010
Hcinaedi|g : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1018
Hacinonych : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1022
Hnemestrin : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1019
Hcholescys : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1000
Hpmatensi : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1020
Hmustelae| : TGTCTAGTTCTCTGACCTGAAACAGGTGCTGCAC : 1020
Hrodentium : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 994
Hpullorum| : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1010
Hfennellia : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1019
Htrogonum : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 994
Hmuridarum : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1015
Hhepaticus : TGTCTGGCTTCTCTGACCTGAAACAGGTGCTGCAC : 976
Hghominis1| : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 989
Hghominis2| : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 993
Hfelis|gb| : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1016
Hbizzozero : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 992
Hsalomonis : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 950
Habutzeri| : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1035
Hcjejuni|gb : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1032
Hsuccinoge : TGTCTAGCTTCTCTGACCTGAAACAGGTGCTGCAC : 1020
TG c gctt c ga C TgaAACAGGTGCTGCAC

```

Figure 1 - 33

		*	1240	*	12	
HbovisR2XA :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1023
Hpylori1gb :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1060
Hbills1gb1 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1227
Hcanis1gb1 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1047
Hcinaedi1g :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1055
Hacinonych :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1059
Hnemestrin :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1056
Hcholescys :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1037
Hpamatensi :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1057
Hmustelae1 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1057
Hrodentium :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1031
Hpullorum1 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1047
Hfennellia :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1056
Htrogontum :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1031
Hmuridarum :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1052
Hhepaticus :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1013
Ghominis11 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1026
Ghominis21 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1030
Hfelis1gb1 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1053
Hbizzozero :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1029
Hsalomonis :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					987
Abutzleri1 :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1072
Cjejunilgb :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1069
Wsuccinoge :	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA :					1057
	GGCTGTCGTCAGCTCGTGCCTGAGATGTTGGGTTAA					

Figure 1 -34

```

60          *          1280          *
HbovisR2XA : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1060
Hpylori1gb : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1097
Hbllis1gb1 : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1264
Hcanis1gb1 : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1084
Hcinaedilg : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1092
Hacinonych : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1096
Hnemestrin : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1093
Hcholescys : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1074
Hpamatensi : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1094
Hmustelae1 : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1094
Hrodentium : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1068
Hpullorum1 : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1084
Hfennellia : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1093
Htrogontum : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1068
Hmuridarum : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1089
Hhepaticus : ----- : 1015
Ghominis11 : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1063
Ghominis21 : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1067
Hfelis1gb1 : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1090
Hbizzozero : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1066
Hsalomonis : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1024
Hbutzlerii : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1109
Cjejunilgb : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1106
Wsuccinoge : GTCCCGCAACGAGCGCAACCCCTCTTCTTAGTTGCTA : 1094
Gtcccgcaacgagcgcaaccctc t cttagtgtcta

```

Figure 1 - 35

```

      1300      *      1320      *
HbovisR2XA : TCAGTTGGGCTGGGCACTCTAAGAGACTGCCTACG : 1096
Hpyloriigb : ACAGGTTATGCTGAGCACTCTAAGAGACTGCCTACG : 1134
Hbilisigb : GCAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1300
Hcanisigb : GCGGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1120
Hcinaedilg : GCAGCTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1128
Hacinonych : ACAGGTTAWGCTGAGCACTCTAAGAGACTGCCTACG : 1133
Hnemestrin : ACAGGTTATGCTGAGCACTCTAAGAGACTGCCTACG : 1129
Hcholescys : GCAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1110
Hpmatensi : ACAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1130
Hmustelae : GCAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1130
Hrodentium : ACTATTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1104
Hpulorum : GCAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1120
Hfennellia : GCAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1129
Htrogonum : GCAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1104
Hmuridarum : GCAGTTGGGCTGAGCACTCTAAGAGACTGCCTACG : 1126
Hhepaticus : -----NNNNNNNNNN----- : 1027
Ghominis1 : ACAGGTTATGCTGGCACTCTAAGAGACTGCCTACG : 1100
Ghominis2 : ACAGGTTATGCTGAGCTCTCTAAGAGACTGCCTACG : 1104
Hfelisigb : ACAGGTTATGCTGAGCTCTCTAAGAGACTGCCTACG : 1127
Hbizzozero : ACAGGTTATGCTGAGCTCTCTAAGAGACTGCCTACG : 1103
Hsalomonis : ACAGGTTATGCTGAGCTCTCTAAGAGACTGCCTACG : 1061
Abutleri : ACAGGTTATGCTGAGCTCTCTAAGAGACTGCCTACG : 1145
Cjejunigb : ACAGGTTATGCTGAGCTCTCTAAGAGACTGCCTACG : 1142
Wsuccinoge : ACAGGTTATGCTGAGCTCTCTAAGAGACTGCCTACG : 1130
      cag t      gctgagcaCTCTAag Agactgcct cg

```

Figure 1 - 36



	1340	*	1360	
HbavisR2XA:	TAACTGGGAGGAAGCTCAGG--CACTCTCAAGTCATCA			: 1133
Hyphorilgb:	TAACTAGGAGCAAGGCTCGGACGAGCTCAAGTCATCA			: 1171
Hbllis gb	TAACTAGGAGGAAGGCTCAGGAGGAGCTTCACAGTCATCA			: 1337
Hcanis gb	TAACTAGGAGGAGGAGCTTACGACGAGCTCAAGTCATCA			: 1157
Hcinaeadi g	TAACTAGGAGGAGGAGCTCAGGACAGCTCAAGTCATCA			: 1165
Hacinonych	TAACTAGGAGGAGGAGCTCGGACGAGCTCAAGTCATCA			: 1170
Hnemestrin	TAACTAGGAGGAGGAGCTCGGACGAGCTCAAGTCATCA			: 1166
Hcholecystr	TAACTAGGAGGAGGAGCTTAGGACGAGCTCAAGTCATCA			: 1147
Hpmatensis	THAGTAGGAGGAGGAGCTTAGGACGAGCTCAAGTCATCA			: 1167
Hmustelael	THAGTAGGAGGAGGAGTATAGGACGAGCTCAAGTCATCA			: 1167
Hrodentium	CAGCTAGGAGGAGGAGCTGAGGACGAGCTCAAGTCATCA			: 1141
Hpallorum	TAACTAGGAGGAGGAGTACGAGACGAGCTCAAGTCATCA			: 1157
Hfennellia	CAGCTAGGAGGAGGAGCTCAGGAGGAGCTCAAGTCATCA			: 1166
Htrogonum	TAACTAGGAGGAGGAGCTCAGGAGGAGCTCAAGTCATCA			: 1141
Hmuridarum	TAACTAGGAGGAGGAGTACGAGGAGCTCAAGTCATCA			: 1163
Hhepaticus	-----HHNNNNNNNNNNNNNNNNNNNNNNNN-----			: 1053
Hgominis1	TAA-----AGGAGAGCTTACGAGGAGCTCAAGTCATCA			: 1133
Hgominis12	TAACTAGGAGGAGGAGCTTAGGAGGAGCTCAAGTCATCA			: 1141
Hfelis gb	TAACTAGGAGGAGGAGCTTAGGAGGAGCTCAAGTCATCA			: 1164
Hblizzozero	TAACTAGGAGGAGGAGCTTAGGAGGAGCTCAAGTCATCA			: 1140
Hsalomonis	TAACTAGGAGGAGGAGCTTAGGAGGAGCTCAAGTCATCA			: 1098
Abutzi1er l	CAGCTAGGAGGAGGAGCTCAGGACGAGCTCAAGTCATCA			: 1182
Cjejun gb	CTAGCTAGGAGGAGGAGCTTAGGAGGAGCTCAAGTCATCA			: 1179
Wsuccinoge	CAGCTAGGAGGAGGAGCTTAGGAGGAGCTCAAGTCATCA			: 1167
	taagtaggaggaaggtgaggacgagctcaagtcattca			

Figure 1 - 37

```

      *          1380          *          1400
HbovisR2XA : TGGCCCTTATGTCGGGGCTACGCACGTGCTACAATG : 1170
Hpylori|gb : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1208
Hbilis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1374
Hcanis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hcinaedi|g : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1202
Hacinonych : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1207
Hnemestrin : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Hcholescys : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1184
Hpmatensi : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hmustelae| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hrodentium : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hpullorum| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hfennellia : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Htrogontum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hmuridarum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1200
Hhepaticus : -----HNE----- : 1057
Ghominis1| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1170
Ghominis2| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hfelis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1201
Hbizzozero : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1177
Hsalomonis : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1135
Hbutzlerii : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1219
Cjejunifgb : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1216
Wsuccinoge : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
tggcccttAcgcctagggctacacacgtgctacaATG

```

Figure 1 - 38

```

      *           1420           *           1440
HbovisR2XA : GGAAGTACAAAGAGAGCAATGTCTAAATGGAGCC : 1207
Hpylori|gb : GGAAGTACAAAGAGAGCAATTTCTGAAATGGAGCC : 1245
Hbilis|gb| : GGAACATACAAAGAGAGTCAATTTGGAGATGGAGCC : 1411
Hcanis|gb| : GGCATACATAGAGAGCAATTTGGAGATGGAGCC : 1231
Hcinaedi|g : GGAACATACAAAGAGAGTCAATTTGGAGATGGAGCC : 1239
Hacinonych : GGTGACAAAGAGAGTCAATTTGGAGATGGAGCC : 1244
Hnemestrin : GGTGACAAAGAGAGTCAATTTGGAGATGGAGCC : 1240
Hcholescys : GTAGTACAAAGAGAGTCAATTTGGAGATGGAGCC : 1221
Hpamatensi : GGAAGTACAAAGAGAGTCAATTTGGAGATGGAGCC : 1241
Hmustelae| : GGTGACAAAGAGAGTCAATTTGGAGATGGAGCC : 1241
Hrodentium : GGAAGTACAAAGAGAGTCAATTTCTGAAATGGAGCC : 1215
Hpullorum| : GGTGACAAAGAGAGTCAATTTCTGAAATGGAGCC : 1231
Hfennellia : GGTGACAAAGAGAGTCAATTTGGAGATGGAGCC : 1240
Htrogontum : GGTGACAAAGAGAGTCAATTTCTGAAATGGAGCC : 1215
Hmuridarum : GGTGACAAAGAGAGTCAATTTCTGAAATGGAGCC : 1237
Hhepaticus : MNMNMNKKHNNNNNNNNNNNNNNNNNNNNNNNNNNNN : 1094
Hhominis1| : GGTGACAAAGAGAGTCAAGAGTCTGAACTAGAGCT : 1207
Hhominis2| : GGTGACAAAGAGAGTCAATGCTGAACTAGAGCT : 1215
Hfelis|gb| : GGTGACAAAGAGAGTCAATGCTGAACTAGAGCT : 1238
Hbizzozero : GGTGACAAAGAGAGTCAATGCTGAACTAGAGCT : 1214
Hsalomonis : GGTGACAAAGAGAGTCAATGCTGAACTAGAGCT : 1172
Habutleri| : GGTGACAAAGAGAGTCAATGCTGAACTAGAGCT : 1256
Hcjejuni|gb : GGTGACAAAGAGAGTCAATGCTGAACTAGAGCT : 1253
Hsuccinoge : GTGACAAAGAGAGTCAATGCTGAACTAGAGCT : 1241
Gg g ACAAagAGa GCaAt G gA gtgGAGC

```

Figure 1 - 39

```

      *               1460               *               1480
HbovisR2XA : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1244
Hpylori|gb : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1282
Hbllis|gb| : AATCTTAAAAATGCTCTCAGTTCGGATTGAGCTG : 1448
Hcanis|gb| : AATCTTAAAAATGCTCTCAGTTCGGATTGAGCTG : 1268
Hcinaedi|g : AATCTTAAAAATGCTCTCAGTTCGGATTGAGCTG : 1276
Hacinonych : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1281
Hnemestrin : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1277
Hcholescys : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1258
Hpmatensi : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1278
Hmustelael : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1278
Hrodentium : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1252
Hpulloruml : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1268
Hfennellia : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1277
Htrogontum : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1252
Hmuridarum : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1274
Hhepaticus : NMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN : 1131
Hghominis1| : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1244
Hghominis2| : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1252
Hfelis|gb| : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1275
Hbizzozero : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1251
Hsalomonis : AATCTTAAAAACGCTCTCAGTTCGGATTGAGGCTG : 1209
Habutzeri| : AATCTTAAAAATGCTCTCAGTTCGGATTGAGCTG : 1293
Cjejunilgb : AATCTTAAAAATGCTCTCAGTTCGGATTGAGCTG : 1290
Wsuccinoge : AATCTTAAAAACGCTCTCAGTTCGGATTGAGCTG : 1278
AATCT AAAAC cTctcAGTTCGGATTG ag CTG

```

Figure 1 - 40

\* 1500 \*

```

HbovisR2XA : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1281
Hpylori|gb : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1319
Hbilis|gb| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1485
Hcanis|gb| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1305
Hcinaedi|g : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1313
Hacinonych : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1318
Hnemestrin : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1314
Hcholescys : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1295
Hpmatensi : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1315
Hmustelae| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1315
Hrodentium : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1289
Hpullorum| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1305
Hfennellia : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1314
Htrogontum : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1289
Hmuridarum : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1311
Hhepaticus : NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN : 1168
Ghominis1| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1281
Ghominis2| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1289
Hfelis|gb| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1312
Hbizzozero : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1288
Hsalomonis : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1246
Abutzleri| : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1330
Cjejunilgb : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1327
Wsuccinoge : CAACTCGGCTG CATGAAGCTGGAATCGCTAGTAATCG : 1315
CAACTCG ct CATGAAGCTGGAATCGCTAGTAATCG

```

Figure 1 - 4|

```

520          *          1540          *
HbovisR2XA : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1318
Hpylori|gb : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1356
Hbilis|gb| : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1522
Hcanis|gb| : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1342
Hcinaedi|g : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1350
Hacinonych : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1355
Hnemestrin : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1351
Hcholescys : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1332
Hpmatensi : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1352
Hmustelae| : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1352
Hrodentium : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1326
Hpullorum| : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1342
Hfennellia : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1351
Htrogontum : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1326
Hmuridarum : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1348
Hhepaticus : NCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1205
Hhominis1| : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1318
Hhominis2| : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1326
Hfelis|gb| : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1349
Hbizzozero : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1325
Hsalomonis : CCAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1283
Hbutzleri| : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1367
Cjejunigb : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1364
Wsuccinoge : TGAATCAGCATATGTCACGGTGAATACGTTCCCGGGTC : 1352
          aATCAGC ATGt CCGTGAATACGTTCCCGGGTC

```

Figure 1 - 42

```

      1560              *              1580              *
HbovisR2XA : TTGTACTCACC---TCA----- : 1335
Hpylori1gb : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1393
Hbilis1gb1 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1559
Hcanis1gb1 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1379
Hcinaedi1g : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1387
Hacinonych : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1392
Hnemestrin : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1388
Hcholescys : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1369
Hpmatensi : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1389
Hmustelae1 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1389
Hrodentium : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1363
Hpullorum1 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1379
Hfennellia : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1388
Htrogontum : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1363
Hmuridarum : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1385
Hhepaticus : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1242
Hghominis1 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1355
Hghominis2 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1363
Hfelis1gb1 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1386
Hbizzozero : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1362
Hsalomonis : TTGTACT----- : 1290
Abutzleri1 : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1404
Cjejuni1gb : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1401
Wsuccinoge : TTGTACTCACCSCCCCGTCACCCATGGGAGTTGTATT : 1389
TTGTACTcaccgcccgtcacaccatgggagttgt tt

```

Figure 1 - 43

```

                                1600          *          1620
HbovisR2XA : ----- : -
Hpylori|gb| : TGCCTTAAGCAGATCTAAATGGTACTGCCAC : 1430
Hbills|gb| : TGCCTTAAGCAGATCTAAATGGTACTGCCAC : 1596
Hcanis|gb| : TGCCTTAAGCAGATCTAAATGGT----- : 1406
Hcinaedi|g : TGCCTTAAGCAGATCTAAATGGTACTGCCAC : 1424
Hacinonych : TGCCTTAAGCAGATCTAAAGCAGTACTGCCAC : 1429
Hnemestrin : TGCCTTAAGCAGATCTAAATACGTACTGCCAC : 1425
Hcholescys : TGCCTTAAGCCAGATCTAAACGGTACGTCCAC : 1406
Hpmatensi : TGCCTTAAGCCAGATCTAAACGGTACGTCCAC : 1426
Hmustelae| : TGCCTTAAGCCAGATCTAAATGGTACGTCCAN : 1426
Hrodentium : TGCCTTAAGCCAGATCTAAACGGTACGTCCAC : 1400
Hpulorum| : TGCCTTAAGCAGATCTAAATCTATANACCAC : 1416
Hfennellia : TGCCTTAAGCCAGATCTAAATGGTACGTCCAC : 1425
Htrogontum : TGCCTTAAGCCAGATCTAAACGGTACGTCCAC : 1400
Hmuridarum : TGCCTTAAGCAGATCTAAATGGTACGTCCAC : 1422
Hhepaticus : TGCCTTAAGCAGATCTAAATGGTACGTCCAC : 1279
Hghominis1| : TGCCTTAAGCAGATCTAAAGCAGTACTGCCAC : 1392
Hghominis2| : TGCCTTAAGCAGATCTAAAGCAGTACTGCCAC : 1400
Hfelis|gb| : TGCCTTAAGCAGATCTAAAGGAGTACTGCCAC : 1423
Hbizzozero : TGCCTTAAGCAGATCTAAAGGAGTACTGCCAC : 1399
Hsalomonis : ----- : -
Abutzleri| : TATTCGAAGCGGATCTAAAGTACTTTCCAC : 1441
Cjejunigb : TATTCGAAGCGGATCTAAATCTACTTTCCAC : 1438
Wsuccinoge : TGCCTTAAGCCAGATCTAAACGGTACTTTCCAC : 1426
gccttaag c g at ctaa t g tac g ccac

```

Figure 1 - 44



		*	1640	*	1660	
HbovisR2XA :	-----	-----	-----	-----	-----	-
Hpylori gb :	GGCAGACACAGCGACTGGG	-----	-----	-----	-----	1450
Hbills gb  :	GGCAGATGAGCGACTGGG	-----	-----	-----	-----	1616
Hcanis gb  :	-----	-----	-----	-----	-----	-
Hcinaedi g :	GGCAGATGAGCGACTGGG	-----	-----	-----	-----	1444
Hacinonych :	GGCAGACACAGCGACTGGG	-----	-----	-----	-----	1449
Hnemestrin :	CGGACACACAGCGACTGGG	TGAAGTCGTAACAAGGT	-----	-----	-----	1462
Hcholescys :	GGCAGATGAGCGACTGGG	-----	-----	-----	-----	1425
Hpmatensi :	GGCAGATGAGCGACTGGG	-----	-----	-----	-----	1446
Hmustelae  :	GGCAGATG	-----	-----	-----	-----	1435
Hrodentium :	GGCAGATGAGCGACTGGG	TGA	-----	-----	-----	1423
Hpullorum  :	GGCAGATGAGG	-----	-----	-----	-----	1428
Hfennellia :	GGCAGATGAGCGACTGGG	-----	-----	-----	-----	1445
Htrogontum :	GGCAGATGAGCGACTGGG	TG	-----	-----	-----	1422
Hmuridarum :	GGCAGATGAGCGACTGGG	-----	-----	-----	-----	1442
Hhepaticus :	GGCAGATGAGCGACTGGG	TGA	-----	-----	-----	1302
Ghominis1  :	GGCAGACACAGCGACTGGG	TG	-----	-----	-----	1414
Ghominis2  :	GGCAGACACAGCGACTGGG	TG	-----	-----	-----	1422
Hfelis gb  :	GGCAGACACAGCGACTGGG	-----	-----	-----	-----	1443
Hbizzozero :	GGCAGACACAGCGACTGGG	TG	-----	-----	-----	1421
Hsalomonis :	-----	-----	-----	-----	-----	-
Abutzleri  :	AGTGGATTGAGYGACTGGG	-----	-----	-----	-----	1461
Cjejuni gb :	AGTGGATTGAGCGACTGGG	-----	-----	-----	-----	1458
Wsuccinoge :	GGCAGATGAGCGACTGGG	-----	-----	-----	-----	1446
	gc a cagcgactggg					

Figure 1 - 45

```

      *
HbovisR2XA : ----- : -
Hpylori|gb : ----- : -
Hbilis|gb| : ----- : -
Hcanis|gb| : ----- : -
Hcinaedi|g : ----- : -
Hacinonych : ----- : -
Hnemestrin : A----- : 1463
Hcholescys : ----- : -
Hpamateni : ----- : -
Hmustelae| : ----- : -
Hrodentium : ----- : -
Hpullorum| : ----- : -
Hfennellia : ----- : -
Htrogontum : ----- : -
Hmuridarum : ----- : -
Hhepaticus : ----- : -
Ghominis1| : ----- : -
Ghominis2| : ----- : -
Hfelis|gb| : ----- : -
Hbizzozero : ----- : -
Hsalomonis : ----- : -
Abutzleri| : ----- : -
Cjejuni|gb : ----- : -
Wsuccinoge : ----- : -

```

Figure 1 - 46

		*	20	*	
Hsuis2BXA0	:	-----			-
Ghominis1l	:	-----		AGTGAACGCT	10
Ghominis2l	:	-----		AGTGAACGCT	10
Hfelislgbl	:	TTTATGGAG		CAGAGTGAACGCT	37
Hbizzozero	:	-----		AGTGAACGCT	10
Hbilislgbl	:	-----		CAGAGTGAACGCT	28
Hsalomonis	:	-----			-
Hpylorilgb	:	TTTATGGAG		CAGAGTGAACGCT	37
Hcanislgbl	:	-----		CAGAGTGAACGCT	28
Hcinaedilg	:	-TTATGGAG		CAGAGTGAACGCT	36
Hacinonych	:	TTTATGGAG		CAGAGTGAACGCT	37
Hnemestrin	:	NNTATGGAG		CAGAGTGAACGCT	37
Hcholescys	:	-----		CAGAGTGAACGCT	18
Hpamatensi	:	-TTATGGAG		CAGAGTGAACGCT	36
Hmustelael	:	ATTATGGAG		CAGAGTGAACGCT	37
Hrodentium	:	-----		CAGAGTGAACGCT	14
Hpulloruml	:	-----		CAGAGTGAACGCT	29
Hfennellia	:	TTTACGGAG		CAGAGTGAACGCT	37
Htrogontum	:	-----		CAGAGTGAACGCT	14
Hmuridarum	:	---ATGGAG		CAGAGTGAACGCT	34
Hhepaticus	:	-----		CAGAGTGAACGCT	13
Abutzleril	:	---ATGGAG		CAGAGTGAACGCT	34
Cjejuni gb	:	--TATGGAG		CAGAGTGAACGCT	35
Wsuccinoge	:	-TTATGGAG		CAGAGTGAACGCT	36
				cagagtgaacgct	

Figure 2 -1

```

      40          *          60          *
Hsuis2BXA0 : -----TGCAAGTCGAACGATGAAG : 19
Ghominis1l : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Ghominis2l : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hfelislgbl : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hbizzozero : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 47
Hbilislgbl : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hsalomonis : -----GAAG : 4
Hpylorilgb : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hcanislgbl : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 65
Hcinaedilg : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 73
Hacinonych : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hnemestrin : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hcholescys : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 55
Hpamatensi : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 73
Hmustelael : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Hrodentium : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hpulloruml : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 66
Hfennellia : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 74
Htrogontum : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 51
Hmuridarum : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 71
Hhepaticus : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 50
Abutzleril : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 72
Cjejunilgb : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 71
Wsuccinoe : GGC GGC GTGCCTAATACATGCAAGTCGAACGATGAAG : 73
          ggcgccgtgcctaataacatgcaagtcgaacgatgag

```

Figure 2 -2

```

      80          *          100          *
Hsuis2BXA0 : C-C-TAGCTTGCTAG---GTT--GATTAGTGGCGCA : 48
Ghominis1| : C-C-TAGCTTGCTAG---TT--GATTAGTGGCGCA : 75
Ghominis2| : C-C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hfelis|gbl : C-C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 103
Hbizzozero : C-C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hbilis|gbl : CTC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 98
Hsalomonis : C-C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 33
Hpylori|gb : CTC-TAGCTTGCTAGAGTGCT---GATTAGTGGCGCA : 108
Hcanis|gbl : CTC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 98
Hcinaedilg : CTC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 106
Hacinonych : CTC-TAGCTTGCTAGAG-GTG--GATTAGTGGCGCA : 107
Hnemestrin : CTCT-TAGCTTGC---ATGCT--GATTAGTGGCGCA : 104
Hcholescys : CTC-TAGCTTGCTAGAGTG--GATTAGTGGCGCA : 88
Hpmatensi : CTCTCTAGCTTGCTAGAGTG--GATTAGTGGCGCA : 108
Hmustelael : CTC-TAGCTTGCTAGAGTG--GATTAGTGGCGCA : 107
Hrodentium : C-TC-TAGCTTGCTAGAGTGG---GATTAGTGGCGCA : 82
Hpullorum| : C-TC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 99
Hfennellia : CTC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 107
Htrogontum : CTC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 84
Hmuridarum : CTC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 104
Hhepaticus : CTC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 83
Abutzleri| : GATTATAGCTTGCTATGATGTCACTAGTGGCGCA : 108
Cjejunigb : C-TC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 105
Wsuccinoge : GGGTCTAGCTTGCTATGCTGCT--GATTAGTGGCGCA : 108
      c      TAGCTTGCTAG      gattAGTGGCGCA

```

Figure 2 - 3

	120	*	140	
Hsuis2BXA0 :	CGGGTGAGTAAAGCATAGT	TG	CATGCCCGTTAGTTT	: 85
Ghominis1l :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 112
Ghominis2l :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 113
Hfelis1gb1 :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 140
Hbizzozero :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 113
Hbilis1gb1 :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 135
Hsalomonis :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 70
Hpylori1gb :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 145
Hcanis1gb1 :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 135
Hcinaedilg :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 143
Hacinonych :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 144
Hnemestrin :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 141
Hcholescys :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 125
Hpmatensi :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 145
Hmustelae1 :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 144
Hrodentium :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 119
Hpullorum1 :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 136
Hfennellia :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 144
Htrogontum :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 121
Hmuridarum :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 141
Hhepaticus :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 120
Abutzleril :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 145
Cjejun1gb :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 142
Wsuccinoge :	CGGGTGAGTAAAGCATAGT	AG	CATGCCCGTTAGTTT	: 145
	CGGGTgAGTAA	GcATAG	T A TGCCc ttAgt t	

Figure 2 - 4

	160	180	
Hsuis2BXA0 :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 122
Ghominis1l :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 149
Ghominis2l :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 150
Hfelis1gb1 :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 177
Hbizzozero :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 150
Hbilis1gb1 :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 172
Hsalomonis :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 107
Hpylori1gb :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 182
Hcanis1gb1 :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 172
Hcinaedilg :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 180
Hacinonych :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 181
Hnemestrin :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 178
Hcholescys :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 162
Hpamatensi :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 182
Hmustelael :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 181
Hrodentium :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 156
Hpulloruml :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 173
Hfennellia :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 181
Htrogontum :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 158
Hmuridarum :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 178
Hhepaticus :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 157
Abutzleril :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 182
Cjejunilgb :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 179
Wsuccinoge :	GGGATAGCCA	TAGAA	TGGTGAATAATAAC : 182

gGgAtAgCca T GAAA GgtgatTAATAC ATAC

Figure 2 - 5

	200	220	
Hsuis2BXA0 :	TACCTT-----	ATGGGGGAAAGA--TTT	: 143
Ghominis1l :	TACCTT-----	ATGGGGGAAAGA--TTT	: 170
Ghominis2l :	TACCTT-----	ATGGGGGAAAGA--TTT	: 171
Hfelislgb :	TACCTT-----	ATGGGGGAAAGA--TTT	: 196
Hblzzozero :	TACCTT-----	ATGGGGGAAAGA--TTT	: 171
Hbilislgb :	TACCTT-----	ATGGGGGAAAGGGGCTTT	: 195
Hsalomonis :	TACCTT-----	ATGGGGGAAAGA--TTT	: 128
Hpylorilgb :	TACCTT-----	ATGGGGGAAAGA--TTT	: 201
Hcanislgb :	TACCTT-----	ATGGGGGAAAG--TTT	: 191
Hcinaedilg :	TACCTT-----	ATGGGGGAAAGG--TTT	: 199
Hacinonych :	TACCTT-----	ATGGGGGAAAGA--TTT	: 200
Hnemestrin :	TACCTT-----	ATGGGGGAAAGA--TTT	: 197
Hcholescys :	TACCTT-----	TACGGGGGAAAG--TTT	: 181
Hpamatensi :	TACCTT-----	TACGGGGGAAAG--TTT	: 201
Hmustelae :	TACCTT-----	ATGGGGGAAAG--NTN	: 200
Hrodentium :	TACCTT-----	ATGGGGGAAAG--TTT	: 175
Hpulloruml :	TACCTT-----	ATGGGGGAAAG--TTT	: 192
Hfennellia :	TACCTT-----	ATGGGGGAAAG--TTT	: 200
Htrogontum :	TACCTT-----	ATGGGGGAAAG--TTT	: 177
Hmuridarum :	TACCTT-----	ATGGGGGAAAG--TTT	: 196
Hhepaticus :	TACCTT-----	ATGGGGGAAAG--TTT	: 176
Abutzleril :	TACCTT-----	ATGGGGGAAAG--TTT	: 216
Cjejunilgb :	TACCTT-----	ATGGGGGAAAG--TTT	: 212
Wsuccinoge :	TACCTT-----	ATGGGGGAAAG--TTT	: 201
	T C	a gggGgAAg TTT	

Figure 2 - 6



	*	240	*	26	
Hsuis2BXA0 :	-----		-----		-
Ghominis1 :	-----		-----		-
Ghominis2 :	-----		-----		-
Hfelis1gb :	-----		-----		-
Hbizzozero :	-----		-----		-
Hbilis1gb :	CAATAAAGAATTTCTCTTTTAGTGCTTTGTTGTT				232
Hsalomonis :	-----		-----		-
Hpylori1gb :	-----		-----		-
Hcanis1gb :	-----		-----		-
Hcinaedi1g :	-----		-----		-
Hacinonych :	-----		-----		-
Hnemestrin :	-----		-----		-
Hcholescys :	-----		-----		-
Hpamatensi :	-----		-----		-
Hmustelae1 :	-----		-----		-
Hrodentium :	-----		-----		-
Hpullorum1 :	-----		-----		-
Hfennellia :	-----		-----		-
Htrogontum :	-----		-----		-
Hmuridarum :	-----		-----		-
Hhepaticus :	-----		-----		-
Hbutzleri1 :	-----		-----		-
Cjejuni1gb :	-----		-----		-
Wsuccinoge :	-----		-----		-

Figure 2 - 7

	0	*	280	*	
Hsuis2BXA0	:	-----	-----	:	-
Ghominis1l	:	-----	-----	:	-
Ghominis2l	:	-----	-----	:	-
Hfelis gb	:	-----	-----	:	-
Hbizzozero	:	-----	-----	:	-
Hbilis gb	:	GGCACAAAATTCTAGTATTGGAAATGAGAAATTGATG	:	269	-
Hsalomonis	:	-----	-----	:	-
Hpylori gb	:	-----	-----	:	-
Hcanis gb	:	-----	-----	:	-
Hcinaedilg	:	-----	-----	:	-
Hacinonych	:	-----	-----	:	-
Hnemestrin	:	-----	-----	:	-
Hcholescys	:	-----	-----	:	-
Hpamatensi	:	-----	-----	:	-
Hmustelae	:	-----	-----	:	-
Hrodentium	:	-----	-----	:	-
Hpullorum	:	-----	-----	:	-
Hfennellia	:	-----	-----	:	-
Htrogontum	:	-----	-----	:	-
Hmuridarum	:	-----	-----	:	-
Hhepaticus	:	-----	-----	:	-
Abutzleri	:	-----	-----	:	-
Cjejuni gb	:	-----	-----	:	-
Wsuccinoge	:	-----	-----	:	-

Figure 2 - 8

	300	*	320	*	
Hsuis2BXA0 :	-----		-----		-
Ghominis1l :	-----		-----		-
Ghominis2l :	-----		-----		-
Hfelislgb :	-----		-----		-
Hbizzozero :	-----		-----		-
Hbllislgb :	TTGTGAAGCAATT	TTGTGCGGAGACTAGACTTAGTGTC			306
Hsalomonis :	-----		-----		-
Hpylorilgb :	-----		-----		-
Hcanislgb :	-----		-----		-
Hcinaedilg :	-----		-----		-
Hacinonych :	-----		-----		-
Hnemestrin :	-----		-----		-
Hcholescys :	-----		-----		-
Hpamatensi :	-----		-----		-
Hmustelael :	-----		-----		-
Hrodentium :	-----		-----		-
Hpulloruml :	-----		-----		-
Hfennellia :	-----		-----		-
Htrogontum :	-----		-----		-
Hmuridarum :	-----		-----		-
Hhepaticus :	-----		-----		-
Abutzleri :	-----		-----		-
Cjejuniigb :	-----		-----		-
Wsuccinoge :	-----		-----		-

Figure 2 -9

	340	*	360	*	
Hsuis2BXA0 :	-----		-----		-
Ghominis1l :	-----		-----		-
Ghominis2l :	-----		-----		-
Hfelis gb  :	-----		-----		-
Hbizzozero :	-----		-----		-
Hbilis gb  :	TGTCGCACAAGCAAATTGCGAACTCATCGATTTATCG				343
Hsalomonis :	-----		-----		-
Hpylori gb :	-----		-----		-
Hcanis gb  :	-----		-----		-
Hcinaedi g :	-----		-----		-
Hacinonych :	-----		-----		-
Hnemestrin :	-----		-----		-
Hcholescys :	-----		-----		-
Hpamatensi :	-----		-----		-
Hmustelae  :	-----		-----		-
Hrodentium :	-----		-----		-
Hpullorum  :	-----		-----		-
Hfennellia :	-----		-----		-
Htrogontum :	-----		-----		-
Hmuridarum :	-----		-----		-
Hhepaticus :	-----		-----		-
Abutzleri  :	-----		-----		-
Cjejunilgb :	-----		-----		-
Wsuccinoge :	-----		-----		-

Figure 2 - 10

	380	A	400	
Hsuis2BXA0 :	-----AT-----		CGCTAAG	: 152
Ghominis1l :	-----AT-----		CGCTAAG	: 179
Ghominis2l :	-----AT-----		CGCTAAG	: 180
Hfelislgbl :	-----AT-----		CGCTAAG	: 205
Hbizzozero :	-----AT-----		CGCTAAG	: 180
Hblislgbl :	TCCAAAGACGAATTTTATTGAAAGCCTT		CGCTAAG	: 380
Hsalomonis :	-----AT-----		CGCTAAG	: 137
Hpylorilgb :	-----AT-----		CGCTAAG	: 210
Hcanislgbl :	-----T-----		CGCTAAG	: 200
Hcinaedilg :	-----T-----		CGCTAAG	: 208
Hacinonych :	-----AT-----		CGCTAAG	: 209
Hnemestrin :	-----AT-----		CGCTAAG	: 206
Hcholescys :	-----TT-----		CGCTAAG	: 190
Hpamatensi :	-----TT-----		CGCTAAG	: 210
Hmustelseel :	-----TT-----		CGCTAAG	: 209
Hrodentium :	-----TT-----		CGCTAAG	: 184
Hpulloruml :	-----TT-----		CGCTAAG	: 201
Hfennellia :	-----TC-----		CGCTAAG	: 209
Htrogontum :	-----TT-----		CGCTAAG	: 186
Hmuridarum :	-----TT-----		CGCTAAG	: 205
Hhepaticus :	-----TT-----		CGCTAAG	: 185
Abutzleril :	-----AT-----		CGCTAAG	: 225
Cjejunilgb :	-----TT-----		CGCTAAG	: 221
Wsuccinoge :	-----TT-----		CGCTAAG	: 210
	t		cGcTa	

Figure 2 - 11

		420		440	
Hsuis2BXA0 :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				189
Ghominis1l :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				216
Ghominis2l :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				217
Hfelis1gbl :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				242
Hbizzozero :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				217
Hbillis1gbl :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				417
Hsalomonis :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				174
Hpylori1gb :	AGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				247
Hcanis1gbl :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				237
Hcinaedilg :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				245
Hacinonych :	AGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				246
Hnemestrin :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				243
Hcholescys :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				227
Hpmatensi :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				247
Hmustelael :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				246
Hrodentium :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				221
Hpulloruml :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				238
Hfennellia :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				246
Htrogontum :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				223
Hmuridarum :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				242
Hhepaticus :	GGATCGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				222
Abutzleri1 :	AGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				262
Cjejunilgb :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				258
Wsuccinoge :	GGATTGGCTATATGTCCTATCAGCTTGTGGTGAGGTA :				247
	ggAT G CTAgtccTATCAGcTtGTTGGTgaGGTA				

Figure 2 - 12

```

      *           460           *           480
Hsuis2BXA0 : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 226
Ghominis1| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 253
Ghominis2| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 254
Hfelis|gb| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 279
Hbizzozero : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 254
Hbilis|gb| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 454
Hsalomonis : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 211
Hpylori|gb| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 284
Hcanis|gb| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 274
Hcinaedilg : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 282
Hacinonych : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 283
Hnemestrin : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 280
Hcholescys : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 264
Hpamateni : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 284
Hmustelae| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 283
Hrodentium : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 258
Hpullorum| : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 275
Hfennellia : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 283
Htrogontum : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 260
Hmuridarum : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 279
Hhepaticus : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 259
Abutzleril : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 299
Cjejunigb : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 295
Wsuccinoge : AAGGCTCACCAGGCTATGACGGGTATCCGGCCTGAG : 284
A gGCTcACCAAGgCtATGACGggtATcCGGcCTGAG

```

Figure 2 - 13

\*                      500                      \*

5

Hsuis2BXA0 : AGGGTGGCGGGACACACTGGAACTGAGACACGGTCCA : 263  
 Ghominis1l : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 290  
 Ghominis2l : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 291  
 Hfelislgb : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 316  
 Hbizzozero : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 291  
 Hbilislgb : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 491  
 Hsalomonis : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 248  
 Hpylorilgb : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 321  
 Hcanislgb : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 311  
 Hcinaedilg : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 319  
 Hacinonych : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 320  
 Hnemestrin : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 317  
 Hcholescys : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 301  
 Hpamatensi : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 321  
 Hmustelae : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 320  
 Hrodentium : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 295  
 Hpullorum : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 312  
 Hfennellia : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 320  
 Htrogontum : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 297  
 Hmuridarum : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 316  
 Hhepaticus : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 296  
 Abuttzleri : AGGATGATCACTCAGACTGGAACTGAGACACGGTCCA : 336  
 Cjejuni1gb : AGGATGATCACTCAGACTGGAACTGAGACACGGTCCA : 332  
 Wsuccinoge : AGGGTGAACGGACACACTGGAACTGAGACACGGTCCA : 321  
 AGGgTGA CgGACACACTGGAACTGAGACACGGTCCA

Figure 2 - 14



	20	40	60	80	100	120	140	160	180	200	220	240	260	280	300
Hsuis2BXA0	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	300										
Ghominis1l	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	327										
Ghominis2l	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	328										
Hfelislgbl	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	353										
Hbizzozero	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	328										
Hbillislgbl	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	528										
Hsalomonis	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	285										
Hpyloriilgb	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	358										
Hcanislgbl	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	348										
Hcinaedilg	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	356										
Hacinonych	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	357										
Hnemestrin	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	354										
Hcholescys	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	338										
Hpmatensi	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	358										
Hmustelae	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	357										
Hrodentium	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	332										
Hpulloruml	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	349										
Hfennellia	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	357										
Htrogonum	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	334										
Hmuridarum	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	353										
Hhepaticus	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	333										
Habutleril	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	373										
Cjejunilgb	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	369										
Wsuccinoge	:	GACTCCTACGGGAGGCAGCAGT	AGGGAATATTGCTCA	:	358										

GACTCCTACGGGAGGCAGCAGT

Figure 2 - 15

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      560          *          580          *
Hsuis2BXA0 : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 337
Ghominis1l : ATGGGCGAAACCTTGGAGCAGCAACGCCCGGTGGAGG : 364
Ghominis2l : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 365
Hfelis|gbl : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 390
Hbizzozero : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 365
Hbillis|gbl : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 565
Hsalomonis : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 322
Hpylori|gb : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 395
Hcanis|gbl : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 385
Hcinaedilg : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 393
Hacinonych : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 394
Hnemestrin : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 391
Hcholescys : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 375
Hpmatensi : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 395
Hmustelael : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 394
Hrodentium : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 369
Hpulloruml : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 386
Hfennellia : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 394
Htrogontum : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 371
Hmuridarum : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 390
Hhepaticus : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 370
Abutzleril : ATGGGCGAAACCTTGAAGCAGCAACGCCCGGTGGAGG : 410
Cjejunilgb : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 406
Wsuccinoge : ATGGGCGAAACCCCTGAAGCAGCAACGCCCGGTGGAGG : 395
ATGGg GaAA ccTGAAGCAGCAACGCCCGGTGGAGG

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Figure 2 - 16

	600	*	620	
Hsuis2BXA0 :	ATGAAGGTTT	TAGGAT	GTAAACTCCTTTT	TAGAG : 374
Ghominis1l :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 401
Ghominis2l :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 402
Hfelis1gb :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 427
Hbizzozero :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 402
Hbilis1gb :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 602
Hsalomonis :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 359
Hpylori1gb :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 432
Hcanis1gb :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 422
Hcinaedi1g :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 430
Hacinonych :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 431
Hnemestrin :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 428
Hcholescys :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 412
Hpamatensi :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 432
Hmustelae :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 431
Hrodentium :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 406
Hpullorum :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 423
Hfennellia :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 431
Hfrogontum :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 408
Hmuridarum :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 427
Hhepaticus :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 407
Abutzleri :	ATGACACATT	TAGGATT	GTAAACTCCTTTT	TAGAG : 447
Cjejun1gb :	ATGACACTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 443
Wsuccinoge :	ATGAAGGTTT	TAGGATT	GTAAACTCCTTTT	TAGAG : 432
	ATGAaggtt	TaGgatt	GTAAACTCCTTTT	T aaga6

Figure 2 - 17

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*           640           *           660
Hsuis2BXA0 : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 410
Ghominis1l : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 437
Ghominis2l : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 438
Hfelis|gb| : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 463
Hbizzozero : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 437
Hbilis|gb| : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 638
Hsalomonis : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 395
Hpylori|gb| : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 468
Hcanis|gb| : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 458
Hcinaedi|g : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 466
Hacinonych : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 467
Hnemestrin : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 464
Hcholescys : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 448
Hpmatensi : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 468
Hmustelae| : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 467
Hrodentium : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 442
Hpullorum| : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 459
Hfennellia : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 467
Htrogontum : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 444
Hmuridarum : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 463
Hhepaticus : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 443
Abutzlerii : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 483
Cjejunigb : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 480
Wsuccinoge : AAGA-TAATGACGGTATCTTAAGGAATAAGCACCGGCT : 468
AAGA T aTGACGGTatct A GAaTAAGCACCGGCT

```

Figure 2 - 18

		680	700	
Hsuis2BXA0	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	447
Ghominis1l	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	474
Ghominis2l	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	475
Hfelis gb	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	500
Hbizzozero	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	474
Hbilis gb	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	675
Hsalomonis	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	432
Hpylori gb	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	505
Hcanis gb	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	495
Hcinaedilg	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	503
Hacinonych	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	504
Hnemestrin	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	501
Hcholescys	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	485
Hpamatensi	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	505
Hmustelael	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	504
Hrodentium	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	479
Hpulloruml	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	496
Hfennellia	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	504
Htrogontum	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	481
Hmuridarum	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	500
Hhepaticus	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	464
Abutzleril	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	520
Cjejunilgb	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	517
Wsuccinoge	:	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC	:	505
		AACTCCGTGCCAGcagcgcggtataacGGAGGGTGC		

Figure 2 - 19

	*	720	*	740	
Hsuis2BXA0 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 484
Ghominis1 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 511
Ghominis2 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 512
Hfelis1gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 537
Hbizzozero :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 511
Hbilis1gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 712
Hsalomonis :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 469
Hpylori1gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 542
Hcanis1gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 532
Hcinaedilg :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 540
Hacinonych :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 541
Hnemestrin :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 538
Hcholescys :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 522
Hpmatensi :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 542
Hmustelael :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 541
Hrodentium :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 516
Hpullorum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 533
Hfennellia :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 541
Htrogonum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 518
Hmuridarum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 537
Hhepaticus :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 501
Habutlerii :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 557
Cjejun1gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 554
Wsuccinoge :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 542
	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				

Figure 2 -20

\*                      760                      \*

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Hsuis2BXA0 : AGGCGGGAGGACAAGTCAGGTGTGAAATCCTATGCT : 521
Ghominis1l : AGGCGGGAGGACAAGTCAGGTGTGAAATCCTATGCT : 548
Ghominis2l : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 549
Hfelis|gb| : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 574
Hbizzozero : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 548
Hbillis|gb| : AGGCGGGAGTAAAGTCAGGTGTGAAATCCTATGAGCT : 749
Hsalomonis : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 506
Hpylori|gb| : AGGCGGGAGTAAAGTCAGGTGTGAAATCCTATGCT : 579
Hcanis|gb| : AGGCGGGAGTAAAGTCAGGTGTGAAATCCTATGAGCT : 569
Hcinaedilg : AGGCGGGTAGTCAAGTCAGGTGTGAAATCCTATGAGCT : 577
Hacinonych : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 578
Hnemestrin : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 575
Hcholescys : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 559
Hpmatensi : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 579
Hmustelae| : AGGCGGGAGTAAAGTCAGGTGTGAAATCCTATGAGCT : 578
Hrodentium : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 553
Hpullorum| : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 570
Hfennellia : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGCT : 578
Htrogonum : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGAGCT : 555
Hmuridarum : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGAGCT : 574
Hhepaticus : AGGCGGGGTTTAAAGTCAGGTGTGAAATCCTATGAGCT : 538
Abutzleril : AGGCGGATTATTAAGTCTTGTGAAATCCTATGAGCT : 594
Cjejunilgb : AGGCGGATTATTAAGTCTTGTGAAATCCTATGAGCT : 591
Wsuccinoge : AGGCGGCTTTTAAAGTCAGGTGTGAAATCCTATGAGCT : 579
AGGCGGg t aAGTCag tGTGAAATcct t GCT

```

Figure 2 -21

```

      780                               800
Hsuis2BXA0 : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 558
Ghominis1| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 585
Ghominis2| : TAACAAAGAACTGCAATTGAAACTGAAACCTAGAG : 586
Hfelis|gb| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 611
Hbizzozero : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 585
Hbillis|gb| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 786
Hsalomonis : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 543
Hpylori|gb| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 616
Hcanis|gb| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 606
Hcinaedi|g : TAACAAAGAACTGCAATTGAAACTGACTATCTGGAG : 614
Hacinonych : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 615
Hnemestrin : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 612
Hcholescys : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 596
Hpamatensi : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 616
Hmustelae| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 615
Hrodentium : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 590
Hpullorum| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 607
Hfennellia : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 615
Htrogonium : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 592
Hmuridarum : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 611
Hhepaticus : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 575
Abutzleri| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 631
Cjejun|gb| : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 628
Wsuccinoge : TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG : 616
TAACAAAGAACTGCAATTGAAACTTCCTTCTGGAG

```

Figure 2 - 22



```

      820          *          840          *
Hsuis2BXA0 : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 595
Ghominis1l : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 622
Ghominis2l : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 623
Hfelis|gb| : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 648
Hbizzozero : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 622
Hbillis|gb| : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 823
Hsalomonis : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 580
Hpylori|gb| : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 653
Hcanis|gb| : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 643
Hcinaedilg : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 651
Hacinonych : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 652
Hnemestrin : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 649
Hcholescys : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 633
Hpmatensi : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 653
Hmustelael : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 652
Hrodentium : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 627
Hpulloruml : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 644
Hfennellia : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 652
Htrogontum : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 629
Hmuridarum : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 648
Hhepaticus : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 612
Habutleri| : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 668
Cje|juni|gb : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 665
Wsuccinoge : T TGGGAGAGGCTAGGTGGAATTCCTGGGTGAGGGGTA : 653
T tGGGAGAGGTAAGTGAATTCtGGGTGAGGGGTA

```

Figure 2 - 23

```

      860          *      880
Hsuis2BXA0 : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 632
Ghominis1l : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 659
Ghominis2l : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 660
Hfelislgb : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 685
Hbizzozero : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 659
Hbilislgb : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 860
Hsalomonis : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 617
Hpylorilgb : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 690
Hcanislgb : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 680
Hcinaedilg : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 688
Hacinonych : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Hnemestrin : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 686
Hcholescys : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 670
Hpamatensi : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 690
Hmustelae : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Hrodentium : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 664
Hpulloruml : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 681
Hfennellia : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 689
Htrogonum : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 666
Hmuridarum : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 685
Hhepaticus : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 649
Habutzeril : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 705
Cjejunilgb : AAATCCGTAGATCAAGAGGAATACTCATTGCGAAG : 702
Wsuccinoge : AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG : 690
      AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG

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Figure 2 - 24

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      *           900           *           920
Hsuis2BXA0 : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 669
Ghominis1l : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 696
Ghominis2l : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 697
Hfelis|gb| : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 721
Hbizzozero : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 696
Hbilis|gb| : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 896
Hsalomonis : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 654
Hpylori|gb : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 727
Hcanis|gb| : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 716
Hcinaedi|g : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 724
Hacinonych : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 726
Hnemestrin : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 723
Hcholescys : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 706
Hpamatensi : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 726
Hmustelae1 : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 725
Hrodentium : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 700
Hpullorum| : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 717
Hfennellia : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 725
Htrogontum : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 702
Hmuridarum : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 721
Hhepaticus : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 685
Abutzleri| : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 741
Cjejuni|gb : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 738
Wsuccinoge : GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA : 726
GCGACCTGCTGGAACAATCACTGACGCTGATTGACCGA

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Figure 2 - 25

	*	940	*	960	
Hsuis2BXA0 :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 706
Ghominis1  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 733
Ghominis2  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 734
Hfelis gb  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 758
Hbizzozero :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 733
Hbillis gb  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 933
Hsalomonis :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 691
Hpylori gb  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 764
Hcanis gb  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 752
Hcinaedilg :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 761
Hacinonych :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 763
Hnemestrin :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 760
Hcholescys :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 743
Hpamatensi :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 763
Hmustelae  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 762
Hrodentium :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 737
Hpullorum  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 753
Hfennellia :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 762
Htrogontum :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 739
Hmuridarum :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 758
Hhepaticus :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 722
Abutzi gb  :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 778
Cje uni gb :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 775
Wsuccinoge :	AAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGTAG				: 763

Figure 2 - 26

	*	980	*	100	
Hsuis2BXA0 :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGAGG	:	743	
Ghominis1  :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGG-AGG	:	769	
Ghominis2  :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGG	:	771	
Hfelis gbl :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGG	:	795	
Hbizzozero :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGG	:	770	
Hbilis gbl :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	970	
Hsalomonis :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGG	:	728	
Hpylori gb :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGAGG	:	801	
Hcanis gbl :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	789	
Hcinaedi g :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	798	
Hacinonych :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGG	:	800	
Hnemestrin :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGAGG	:	797	
Hcholescys :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGT	:	780	
Hpamatensi :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGAG	:	800	
Hmustelae  :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGT	:	799	
Hrodentium :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGAG	:	774	
Hpullorum  :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGAG	:	790	
Hfennellia :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	799	
Htrogontum :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	776	
Hmuridarum :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	795	
Hhepaticus :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	759	
Abutzlerii :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGAG	:	815	
Cjejunii gb :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGGGGT	:	812	
Wsuccinogae :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTGCCCTG	:	800	
	TCCACGCCCTAAACGATG	AtGCTAGTTGTTG	G		

Figure 2 - 27

	0	*	1020	*	
Hsuis2BXA0 :	CTT	GTCTTTT	CAGTAATGCAGCTAACGGC	TTAAGCA	: 780
Ghominis1l :	CTT	GTCTTTT	CAGTAATGC	CGTAACGGC	TTAAGCA : 806
Ghominis2l :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 808
Hfelis gbl :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 831
Hbizzozero :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 807
Hbillis gbl :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 1006
Hsalomonis :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 765
Hpylori gb :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 838
Hcanis gbl :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 825
Hcinaedilg :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 834
Hacinonych :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 837
Hnemestrin :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 834
Hcholescys :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 816
Hpmatensi :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 836
Hmustelae :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 835
Hrodentium :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 810
Hpullorum :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGCA	: 826
Hfennellia :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 835
Htrogontum :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 812
Hmuridarum :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 831
Hhepaticus :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 795
Habutzeril :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGTG	: 851
Cjejunigb :	CTT	GTCTCTC	CAGTAATGCAGCTAACGGC	TTAAGTG	: 848
Wsuccinoge :	CTT	GTCTGGG	CAGTAATGCAGCTAACGGC	TTAAGCA	: 836
	CTC	GtC	CAGTAATGCAGCTAACGc	TTAAGca	

Figure 2 - 28

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      1040          *          1060          *
Hsuis2BXA0 : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 817
Ghominis1l : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 842
Ghominis2l : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 845
Hfelis|gb| : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 868
Hbizzozero : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 844
Hbillis|gb| : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 1043
Hsalomonis : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 802
Hpylori|gb| : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 875
Hcanis|gb| : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 862
Hcinaedilg : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 871
Hacinonych : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 874
Hnemestrin : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 871
Hcholescys : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 853
Hpamatensi : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 873
Hmustelael : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 872
Hrodentium : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 847
Hpulloruml : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 863
Hfennellia : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 872
Htrogontum : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 849
Hmuridarum : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 868
Hhepaticus : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 832
Abutzleril : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 888
Cjejunilgb : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 885
Wsuccinoge : TCCGCCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA : 873
T CCGCCTGGGGAGTACGGTCGCAAGATTAAAAC TCA

```

Figure 2 - 29

	1080	*	1100	*	
Hsuis2BXA0 :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 854
Ghominis1l :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 878
Ghominis2l :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 882
Hfelis1gb1 :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 905
Hbizzozero :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 881
Hbilis1gb1 :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 1080
Hsalomonis :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 839
Hpylori1gb :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 912
Hcanis1gb1 :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 899
Hcinaedilg :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 908
Hacinonych :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 911
Hnemestrin :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 908
Hcholescys :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 890
Hpamatensi :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 910
Hmustelael :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 909
Hrodentium :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 884
Hpulloruml :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 900
Hfennellia :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 909
Htrogontum :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 886
Hmuridarum :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 905
Hhepaticus :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 869
Abutzlerij :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 925
Cjejun1gb :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 922
Wsuccinoge :	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			: 910
	AAGGAATAGACGGGGAC	CGGCACAAGCGGTGGAGCAT			

Figure 2 - 30



```

      1120          *          1140
Hsuis2BXA0 : GTGGTTTAATTGGAAGTACCGAAGAACCTTACCTA : 891
Ghominis1l : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 915
Ghominis2l : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 919
Hfelislgb : GTGGTTTAATTGGAANNXXACCGAAGAACCTTACCTA : 942
Hbizzozero : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 918
Hbilislgb : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 1117
Hsalomonis : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 876
Hpylorilgb : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 949
Hcanislgb : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 936
Hcinaedilg : GTGGTTTAATTGGAAGTACCGAAGAACCTTACCTA : 945
Hacinonych : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 948
Hnemestrin : GTGGTTTAATTGGAAGTACCGAAGAACCTTACCTA : 945
Hcholescys : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 927
Hpamatensi : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 947
Hmustelae : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 946
Hrodentium : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 921
Hpullorum : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 937
Hfennellia : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 946
Htrogontum : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 923
Hmuridarum : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 942
Hhepaticus : GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA : 906
Abutzleril : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 962
Cjejuni1gb : GTGGTTTAATTGGAAGNATACCGAAGAACCTTACCTA : 959
Wsuccinoge : GTGGTTTAATTGGAANNHACCGAAGAACCTTACCTA : 947
GTGGTTTAATTGGAAGATACCGAAGAACCTTACCTA

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Figure 2 -31

```

      *           1160           *           1180
Hsuis2BXA0 : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 928
Ghominis1l : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 952
Ghominis2l : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 956
Hfelis|gb| : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 979
Hbizzozero : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 955
Hbilis|gb| : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 1154
Hsalomonis : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 913
Hpylori|gb : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 986
Hcanis|gb| : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 973
Hcinaedilg : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 982
Hacinonych : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 985
Hnemestrin : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 982
Hcholescys : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 964
Hpmatensi : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 984
Hmustelae| : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 983
Hrodentium : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 958
Hpullorum| : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 974
Hfennellia : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 983
Htrogontum : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 960
Hmuridarum : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 979
Hhepaticus : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 943
Abutzler| : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 999
Cjejun|gb : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 996
Wsuccinoge : GGCTTGACATTGAGGAATTCCTAGAAATAGGGGAG : 984
GgCTTGAcATTga aGAAtc cTAGA ATAg ggag

```

Figure 2 - 32

		1200		1220	
Hsuis2BXA0 :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	965
Ghominis1l :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	989
Ghominis2l :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	993
Hfelis1gbl :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	1016
Hbizzozero :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	992
Hbilis1gbl :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	1190
Hsalomonis :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	950
Hpylori1gbl :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	1023
Hcanis1gbl :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	1010
Hcinaedilg :	TG-TGGCTT	CCAGAC	CTGAAAACAGGTGCTGCAC	:	1018
Hacinonych :	TCTCTAGCCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	1022
Hnemestrin :	TCTCTGGCTT	TACAGAC	CTGAAAACAGGTGCTGCAC	:	1019
Hcholescys :	TG-CTGGCTT	CCAGAC	CTGAAAACAGGTGCTGCAC	:	1000
Hpamatensi :	TG-CTGGCTT	CCAGAC	CTGAAAACAGGTGCTGCAC	:	1020
Hmustelael :	TCTCTAGCTT	TACAGAC	CTGAAAACAGGTGCTGCAC	:	1020
Hrodentium :	TG-CTAGCCTT	CCAGAC	CTGAAAACAGGTGCTGCAC	:	994
Hpulloruml :	TG-CTAGCCTT	CCAGAC	CTGAAAACAGGTGCTGCAC	:	1010
Hfennellia :	TG-CTAGCCTT	CCAGAC	CTGAAAACAGGTGCTGCAC	:	1019
Htrogonum :	TG---CCCTTCGGG	CCAGAC	CTGAAAACAGGTGCTGCAC	:	994
Hmuridarum :	TG-CCACTTCTGGG	CCAGAC	CTGAAAACAGGTGCTGCAC	:	1015
Hhepaticus :	TG---CCTTCGGG	CCAGAC	CTGAAAACAGGTGCTGCAC	:	976
Abutzleril :	TG-TCTGCTT	CAGAC	CTGAAAACAGGTGCTGCAC	:	1035
Cjejun1gbl :	TG-CTAGCCTT	CCAGAC	CTGAAAACAGGTGCTGCAC	:	1032
Wsuccinoge :	TG-CCGCTT	TACAGAC	CTGAAAACAGGTGCTGCAC	:	1020
	TG	ct	gcTt	c	aga
					C TgaAaACAGGTGCTGCAC

Figure 2 - 33

	*	1240	*	12	
Hsuis2BXA0 :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1002
Ghominis1l :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1026
Ghominis2l :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1030
Hfelisjgb :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1053
Hbizzozero :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1029
Hbilisjgb :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1227
Hsalomonis :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 987
Hpyloriigb :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1060
Hcanisjgb :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1047
Hcinaedilg :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1055
Hacinonych :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1059
Hnemestrin :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1056
Hcholescys :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1037
Hpmatensi :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1057
Hmustelae :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1057
Hrodentium :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1031
Hpulloruml :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1047
Hfennellia :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1056
Htrogontum :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1031
Hmuridarum :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1052
Hhepaticus :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1013
Abutzleri :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1072
Cjejunigb :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1069
Wsuccinoge :	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	: 1057
	GGCTGTCGT	CAGCTCGT	GTCGTGAGATGT	GGGTTAA	

Figure 2 - 34

```

60          *          1280          *
Hsuis2BXA0 : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1039
Ghominis1 : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1063
Ghominis2 : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1067
Hfelis1gb : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1090
Hbizzozero : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1066
Hbillis1gb : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1264
Hsalomonis : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1024
Hpylori1gb : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1097
Hcanis1gb : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1084
Hcinaedilg : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1092
Hacinonych : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1096
Hnemestrin : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1093
Hcholescys : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1074
Hpamatensi : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1094
Hmustelael : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1094
Hrodentium : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1068
Hpullorum : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1084
Hfennellia : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1093
Htrogontum : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1068
Hmuridarum : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1089
Hhepaticus : N----- : 1015
Abutzleri : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1109
Cjejun1gb : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1106
Wsuccinoge : GTCCCGCAACGAGCGCAACCCCTTTCTTAGTTGCTA : 1094
Gtcccgcaacgagcgcaaccctc t cttagtgtgcta

```

Figure 2 - 35

```

      1300          *          1320          *
Hsuis2BXA0 : GCAGGTATGCTGCTGCACCTCTAAGAGACTGCCTCGG : 1076
Ghominis1l : GCAGGTATGCTGCTGCACCTCTAAGAGACTGCCTCGG : 1100
Ghominis2l : GCAGGTATGCTGCTGAGCTCTCTAAGAGACTGCCTCGG : 1104
Hfelis|gb| : GCAGGTATGCTGCTGAGCTCTCTAAGAGACTGCCTCGG : 1127
Hbizzozero : GCAGGTATGCTGCTGAGCTCTCTAAGAGACTGCCTCGG : 1103
Hbilis|gb| : GCAGTTTGGCTGAGCACTCTAAGAGACTGCCTCGG : 1300
Hsalomonis : GCAGGTATGCTGCTGAGCTCTCTAAGAGACTGCCTCGG : 1061
Hpylori|gb| : GCAGGTATGCTGCTGAGCACTCTAAGAGACTGCCTCGG : 1134
Hcanis|gb| : GCAGTTTGGCTGAGCACTCTAAGAGACTGCCTCGG : 1120
Hcinaedilg : GCAGTTTGGCTGAGCACTCTAAGAGACTGCCTCGG : 1128
Hacinonych : GCAGGTATGCTGCTGAGCACTCTAAGAGACTGCCTCGG : 1133
Hnemestrin : GCAGGTATGCTGCTGAGCACTCTAAGAGACTGCCTCGG : 1129
Hcholescys : GCAGTTTGGCTGAGCACTCTCTAGAGACTGCCTCGG : 1110
Hpamatensi : GCAGTTTGGCTGAGCACTCTCTAGAGACTGCCTCGG : 1130
Hmustelael : GCAGTTTGGCTGAGCACTCTCTAGAGACTGCCTCGG : 1130
Hrodentium : GCATTTTGGTAGAGCACTCTAAGAGACTGCCTCGG : 1104
Hpulloruml : GCAGTTTGGCTGAGCACTCTCTAGAGACTGCCTCGG : 1120
Hfennellia : GCAGTTTGGCTGAGCACTCTCTAGAGACTGCCTCGG : 1129
Htrogontum : GCAGTTTGGCTGAGCACTCTCTAGAGACTGCCTCGG : 1104
Hmuridarum : GCAGTTTGGCTGAGCACTCTAAGAGACTGCCTCGG : 1126
Hhepaticus : -----NNNNNNNNNN----- : 1027
Abutzi1eril : GCAGTTTGGCTGAGCACTCTAAGAGACTGCCTCGG : 1145
Cjejunilgb : CGGCTTGGCTGAGCACTCTAAGAGACTGCCTCGG : 1142
Wsuccinoge : GCAGTTTGGCTGAGCACTCTAAGAGACTGCCTCGG : 1130
cag t gctgagcaCTCTAag Agactgcct cg

```

Figure 2 - 36

Figure 2 - 37

```

      *           1380           *           1400
Hsuis2BXA0 : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1150
Ghominis1l : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1170
Ghominis2l : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hfelislgbl : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1201
Hbizzozero : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1177
Hbilislgbl : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1374
Hsalomonis : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1135
Hpylorilgb : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1208
Hcanislgbl : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hcinaedilg : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1202
Hacinonych : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1207
Hnemestrin : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Hcholescys : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1184
Hpmatensi : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hmustelael : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hrodentium : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hpulloruml : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hfennellia : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Htrogontum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hmuridarum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1200
Hhepaticus : -----N-----NNN : 1057
Abutzleri : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1219
Cjejuni : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1216
Wsuccinoge : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
tggcccttAcgcctagggtacacacgtgctacaATG

```

Figure 2 - 38



```

      *           1420           *           1440
Hsuis2BXA0 : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1187
Ghominis1l : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1207
Ghominis2l : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1215
Hfelislgb : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1238
Hbizzozero : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1214
Hbilislgb : GGACATACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1411
Hsalomonis : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1172
Hpylorilgb : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1245
Hcanislgb : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1231
Hcinaedilg : GGACATACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1239
Hacinonych : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1244
Hnemestrin : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1240
Hcholescys : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1221
Hpmatensi : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1241
Hmustelae : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1215
Hrodentium : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1231
Hpulloruml : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1240
Hfennellia : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1215
Htrogontum : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1237
Hmuridarum : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1094
Hhepaticus : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1256
Abutzleri : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1253
Cjejunilgb : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1241
Wsuccinoge : GGATGACAAAGAGATCCAAAGCGGAGAGCAAGATT : 1241
Gg g ACAaagAGa GCaAt c G GA gtgGAGC

```

Figure 2 - 39

```

      *               1460               *               1480
Hsuis2BXA0 : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1224
Ghominis1| : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1244
Ghominis2| : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1252
Hfelis1gb| : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1275
Hbizzozero : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1251
Hbilis1gb| : AATCTATAAACTGCTCTCAGTTCGGATTGAGGCTG : 1448
Hsalomonis : AATCTATAAAAGGGCTCTCAGTTCGGATTGAGGCTG : 1209
Hpylori1gb : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1282
Hcanis1gb| : AATCTCTAAATGCTCTCAGTTCGGATTGAGGCTG : 1268
Hcinaedilg : AATCTCTAAATGCTCTCAGTTCGGATTGAGGCTG : 1276
Hacinonych : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1281
Hnemestrin : AATCTATAAAACGCTCTCAGTTCGGATTGAGGCTG : 1277
Hcholescys : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1258
Hpamatensi : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1278
Hmustelae| : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1278
Hrodentium : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1252
Hpullorum| : AATCTATAAAACCTCTCAGTTCGGATTGAGGCTG : 1268
Hfennellia : AATCTATAAAAGGCTCTCAGTTCGGATTGAGGCTG : 1277
Htrogonum : AATCTATAAAAGGCTCTCAGTTCGGATTGAGGCTG : 1252
Hmuridarum : AATCTCTAAAAACCTCTCAGTTCGGATTGAGGCTG : 1274
Hhepaticus : NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN : 1131
Abutzleri| : AATCTATAAAATGCTCTCAGTTCGGATTGAGGCTG : 1293
Cjejun1gb : AATCTATAAAATGCTCTCAGTTCGGATTGAGGCTG : 1290
Wsuccinoge : AATCTTTAAAAACCTCTCAGTTCGGATTGAGGCTG : 1278
      AATCT  AAAAC  CTCTcAGITCGGATTG ag CTG

```

Figure 2 -40

```

                                *           *           1
                                1500
Hsuis2BXA0 : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1261
Ghominis1l : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1281
Ghominis2l : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1289
Hfelis1gb| : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1312
Hbizzozero : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1288
Hbillis1gb| : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1485
Hsalomonis : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1246
Hpylori1gb| : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1319
Hcanis1gb| : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1305
Hcinaedilg : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1313
Hacinonych : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1318
Hnemestrin : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1314
Hcholescys : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1295
Hpmatensi : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1315
Hmustelael : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1315
Hrodentium : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1289
Hpulloruml : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1305
Hfennellia : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1314
Htrogontum : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1289
Hmuridarum : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1311
Hhepaticus : NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN : 1168
Abutzleril : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1330
Cejuni1gb| : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1327
Wsuccinoge : CAACTCGCTGCTGATGAAGCTGGAATCGCTAGTAATCG : 1315
CAACTCG ct CATgAAGCTGGAATCGCTAGTAATCG

```

Figure 2 - 41

```

520          *          1540          *
Hsuis2BXA0 : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1298
Ghominis1l : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1318
Ghominis2l : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1326
Hfelis1gbl : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1349
Hbizzozero : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1325
Hbilis1gbl : TGAATCAGCAATGTACGGTGAATACGTTCCCGGGTC : 1522
Hsalomonis : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1283
Hpylori1gb : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1356
Hcanis1gbl : TGAATCAGCAATGTACGGTGAATACGTTCCCGGGTC : 1342
Hcinaed1lg : AATCAGCAATGTGCGGTGAATACGTTCCCGGGTC : 1350
Hacinonych : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1355
Hnemestrin : ATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1351
Hcholescys : TGAATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1332
Hpamatenisi : TGAATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1352
Hmustelael : TGAATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1352
Hrodentium : TATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1326
Hpulloxum1 : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1342
Hfennellia : AATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1351
Htrogontum : AATCAGCAATGTGCGGTGAATACGTTCCCGGGTC : 1326
Hmuridarum : TGAATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1348
Hhepaticus : AATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1205
Abutzleril : TATCAGCATGTGCGGTGAATACGTTCCCGGGTC : 1367
Cjejun1gbl : TATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1364
Wsuccinoge : TATCAGCATGTACGGTGAATACGTTCCCGGGTC : 1352
          aATCAGCATGTGCGGTGAATACGTTCCCGGGTC

```

Figure 2 - 42

```

      1560          *          1580          *
Hsuis2BXA0 : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1335
Ghominis1l : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1355
Ghominis2l : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1363
Hfelislgb| : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1386
Hbizzozero : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1362
Hbilislgb| : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1559
Hsalomonis : TTGTAAT----- : 1290
Hpylorilgb : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1393
Hcanislgb| : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1379
Hcinaedilg : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1387
Hacinonych : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1392
Hnemestrin : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1388
Hcholescys : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1369
Hpmatensi : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1389
Hmustelael : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1389
Hrodentium : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1363
Hpulloruml : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1379
Hfennellia : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1388
Htrogontum : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1363
Hmuridarum : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1385
Hhepaticus : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1242
Abutzleril : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1404
Cjejunilgb : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1401
Wsuccinoge : TTGTAATCACC GCCCGTCACACCATGGGAGTTGTGTT : 1389
TTGTAATcaccgcccgtcacaccatgggagttgtt tt

```

Figure 2 - 43

```

          1600          *          1620
Hsuis2BXA0 : TGCCTTAAGCAGGATCTAAAGCAGGTACTGCGCCAC : 1372
Ghominis1l : TGCCTTAAGCAGGATCTAAAGCAGGTACTGCGCCAC : 1392
Ghominis2l : TGCCTTAAGCAGGATCTAAAGCAGGTACTGCGCCAC : 1400
Hfellis|gb| : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1423
Hbizzozero : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1399
Hbllis|gb| : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1596
Hsalomonis : ----- : -
Hpylori|gb| : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1430
Hcanis|gb| : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1406
Hcinaedilg : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1424
Hacinonych : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1429
Hnemestrin : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1425
Hcholescys : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1406
Hpmatensi : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1426
Hmustelael : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1426
Hrodentium : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1400
Hpulloruml : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1416
Hfennellia : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1425
Htrogontum : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1400
Hmuridarum : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1422
Hhepaticus : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1279
Habutzeril : TATTCGAACCGGATCTAAAGGAGGTACTGCGCCAC : 1441
Cjejunigb : TATTCGAACCGGATCTAAAGGAGGTACTGCGCCAC : 1438
Wsuccinoge : TGCCTTAAGCAGGATCTAAAGGAGGTACTGCGCCAC : 1426
gccttaag c g at ctaaa t g tac g ccac

```

Figure 2 - 44

```

      *           1640           *           1660
Hsuis2BXA0 : GGCACACACAGCGACTGGGGTGAAGTCGTAACAAGGT : 1409
Ghominis1l : GGCACACACAGCGACTGGGGTG----- : 1414
Ghominis2l : GGCACACACAGCGACTGGGGTG----- : 1422
Hfelislgb| : GGCACACACAGCGACTGGGG----- : 1443
Hbizzozero : GGCACACACAGCGACTGGGGTG----- : 1421
Hbilislgb| : GGCACACAGCGACTGGGG----- : 1616
Hsalomonis : ----- : -
Hpylorilgb : GGCACACACAGCGACTGGGG----- : 1450
Hcanislgb| : ----- : -
Hcinaedilg : GGCACACAGCGACTGGGG----- : 1444
Hacinonych : GGCACACACAGCGACTGGGG----- : 1449
Hnemestrin : GGCACACACAGCGACTGGGGTGAAGTCGTAACAAGGT : 1462
Hcholescys : GGCACACAGCGACTGGG----- : 1425
Hpamatensi : GGCACACAGCGACTGGGG----- : 1446
Hmustelae| : GGCACACAGCGACTGGGG----- : 1435
Hrodentium : GGCACACAGCGACTGGGGTGA----- : 1423
Hpullorum| : GGCACACAGCGACTGGGG----- : 1428
Hfennellia : GGCACACAGCGACTGGGG----- : 1445
Htrogontum : GGCACACAGCGACTGGGGTG----- : 1422
Hmuridarum : GGCACACAGCGACTGGGG----- : 1442
Hhepaticus : GGCACACAGCGACTGGGGTGA----- : 1302
Abutzleril : GGCACACAGCGACTGGGG----- : 1461
Cjejunilgb : GGCACACAGCGACTGGGG----- : 1458
Wsuccinoge : GGCACACAGCGACTGGGG----- : 1446
ggc a cagcgactgggg

```

Figure 2 - 45

```

      *
Hsuis2BXA0 : AACCCGGGCGGC : 1421
Ghominis1l : ----- : -
Ghominis2l : ----- : -
Hfelis|gb| : ----- : -
Hbizzozero : ----- : -
Hbilis|gb| : ----- : -
Hsalomonis : ----- : -
Hpylori|gb : ----- : -
Hcanis|gb| : ----- : -
Hcinaedilg : ----- : -
Hacinonych : ----- : -
Hnemestrin : A----- : 1463
Hcholescys : ----- : -
Hpamatensi : ----- : -
Hmustelae| : ----- : -
Hrodentium : ----- : -
Hpullorum| : ----- : -
Hfennellia : ----- : -
Htrogontum : ----- : -
Hmuridarum : ----- : -
Hhepaticus : ----- : -
Abutzleril : ----- : -
Cjejuni|gb : ----- : -
Wsuccinoge : ----- : -

```

Figure 2 - 46



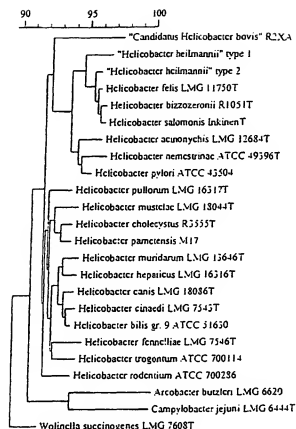


Fig 3A

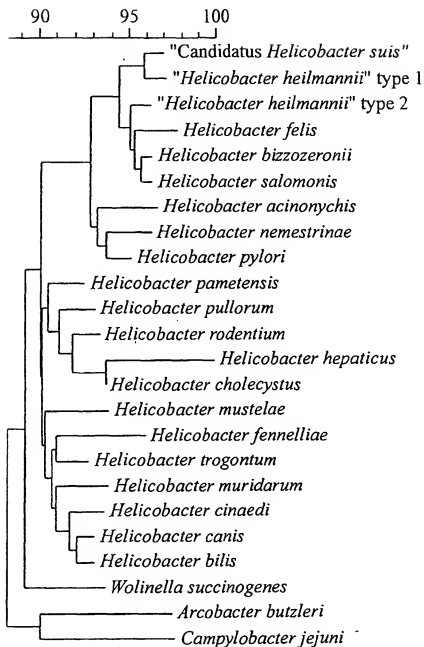


Fig 3B

R2XA001	ACGCTGGCGG	CGTGCCTAAT	ACATGCAAGT	CGATGCAAGT	CGATGCAAGT
R5XE001	ACGCTGGCGG	CGTGCCTAAT	ACATGCAAGT	CGATGCAAGT	CGATGCAAGT
R3XA001	ACGCTGGCGG	CGTGCCTAAT	ACATGCAAGT	CGATGCAAGT	CGATGCAAGT
R6XA001	.....	.....	.....	.....	.....
R13D001INV	.....	.....	.....	.....	.....
R27TOTAAL	.....	.....	.....	.....	.....
R28TOTAAL	.....	.....	.....	.....	.....
R2XA001	.....	.....	.....	.....	.....
R5XE001	.....	.....	.....	.....	.....
R3XA001	.....	.....	.....	.....	.....
R6XA001	.....	.....	.....	.....	.....
R13D001INV	.....	.....	.....	.....	.....
R27TOTAAL	.....	.....	.....	.....	.....
R28TOTAAL	.....	.....	.....	.....	.....
R2XA001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAAATA	CTAGATACGC
R5XE001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAAATA	CTAGATACGC
R3XA001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAAATA	CTAGATACGC
R6XA001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAAATA	CTAGATACGC
R13D001INV	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAAATA	CTAGATACGC
R27TOTAAL	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAAATA	CTAGATACGC
R28TOTAAL	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAAATA	CTAGATACGC
R2XA001	CCTAAGGGGG	AAAGAATTTC	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R5XE001	CCTAAGGGGG	AAAGAATTTC	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R3XA001	CCTAAGGGGG	AAAGAATTTC	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R6XA001	CCTAAGGGGG	AAAGAATTTC	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R13D001INV	CCTAAGGGGG	AAAGAATTTC	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R27TOTAAL	CCTAAGGGGG	AAAGAATTTC	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R28TOTAAL	CCTAAGGGGG	AAAGAATTTC	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R2XA001	AGTTGGTGAG	GTAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R5XE001	AGTTGGTGAG	GTAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R3XA001	AGTTGGTGAG	GTAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R6XA001	AGTTGGTGAG	GTAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R13D001INV	AGTTGGTGAG	GTAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R27TOTAAL	AGTTGGTGAG	GTAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R28TOTAAL	AGTTGGTGAG	GTAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R2XA001	AGGGTGAACG	GACACACCGG	AACAGGAC	CGGTCCGGAC	TCTACGGGA
R5XE001	AGGGTGAACG	GACACACCGG	AACAGGAC	CGGTCCGGAC	TCTACGGGA
R3XA001	AGGGTGAACG	GACACACCGG	AACAGGAC	CGGTCCGGAC	TCTACGGGA
R6XA001	AGGGTGAACG	GACACACCGG	AACAGGAC	CGGTCCGGAC	TCTACGGGA
R13D001INV	AGGGTGAACG	GACACACCGG	AACAGGAC	CGGTCCGGAC	TCTACGGGA
R27TOTAAL	AGGGTGAACG	GACACACCGG	AACAGGAC	CGGTCCGGAC	TCTACGGGA
R28TOTAAL	AGGGTGAACG	GACACACCGG	AACAGGAC	CGGTCCGGAC	TCTACGGGA

Figure 4 - 1

R2XA001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTG	AGCAGCAACG
R5XE001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTG	AGCAGCAACG
R3XA001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTG	AGCAGCAACG
R6XA001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTG	AGCAGCAACG
R13D001INV	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTG	AGCAGCAACG
R27TOTAAL	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTG	AGCAGCAACG
R28TOTAAL	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTG	AGCAGCAACG
R2XA001	CCGCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R5XE001	CCGCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R3XA001	CCGCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R6XA001	CCGCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R13D001INV	CCGCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R27TOTAAL	CCGCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R28TOTAAL	CCGCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R2XA001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R5XE001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R3XA001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R6XA001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R13D001INV	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R27TOTAAL	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R28TOTAAL	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R2XA001	CCGCGGTAAAT	ACGGAGGGTG	CAAAACGTTAC	TCGGAATCAC	TGGGCGTAAAT
R5XE001	CCGCGGTAAAT	ACGGAGGGTG	CAAAACGTTAC	TCGGAATCAC	TGGGCGTAAAT
R3XA001	CCGCGGTAAAT	ACGGAGGGTG	CAAAACGTTAC	TCGGAATCAC	TGGGCGTAAAT
R6XA001	CCGCGGTAAAT	ACGGAGGGTG	CAAAACGTTAC	TCGGAATCAC	TGGGCGTAAAT
R13D001INV	CCGCGGTAAAT	ACGGAGGGTG	CAAAACGTTAC	TCGGAATCAC	TGGGCGTAAAT
R27TOTAAL	CCGCGGTAAAT	ACGGAGGGTG	CAAAACGTTAC	TCGGAATCAC	TGGGCGTAAAT
R28TOTAAL	CCGCGGTAAAT	ACGGAGGGTG	CAAAACGTTAC	TCGGAATCAC	TGGGCGTAAAT
R2XA001	GAGCGGTGAG	CCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAAC
R5XE001	GAGCGGTGAG	CCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAAC
R3XA001	GAGCGGTGAG	CCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAAC
R6XA001	GAGCGGTGAG	CCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAAC
R13D001INV	GAGCGGTGAG	CCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAAC
R27TOTAAL	GAGCGGTGAG	CCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAAC
R28TOTAAL	GAGCGGTGAG	CCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAAC
R2XA001	GCGGAACTGC	GTTTGAACCT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R5XE001	GCGGAACTGC	GTTTGAACCT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R3XA001	GCGGAACTGC	GTTTGAACCT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R6XA001	GCGGAACTGC	GTTTGAACCT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R13D001INV	GCGGAACTGC	GTTTGAACCT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R27TOTAAL	GCGGAACTGC	GTTTGAACCT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R28TOTAAL	GCGGAACTGC	GTTTGAACCT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG

Figure 4 - 2

R2XA001	AACCTCTTGGT	GTAGGGGTAA	AATCCGTAGA	TATCAAGAAG	AATACTCATT
R5XE001	AACCTCTTGGT	GTAGGGGTAA	AATCCGTAGA	TATCAAGAAG	AATACTCATT
R3XA001	AACCTCTTGGT	GTAGGGGTAA	AATCCGTAGA	TATCAAGAAG	AATACTCATT
R6XA001	AACCTCTTGGT	GTAGGGGTAA	AATCCGTAGA	TATCAAGAAG	AATACTCATT
R13D001INV	AACCTCTTGGT	GTAGGGGTAA	AATCCGTAGA	TATCAAGAAG	AATACTCATT
R27TOTAAL	AACCTCTTGGT	GTAGGGGTAA	AATCCGTAGA	TATCAAGAAG	AATACTCATT
R28TOTAAL	AACCTCTTGGT	GTAGGGGTAA	AATCCGTAGA	TATCAAGAAG	AATACTCATT
R2XA001	GCGAAGGC	CCTGCTGGAA	CAT <sup>2</sup> ACTGAC	GCTGATGCCG	GAAAGC <sup>3</sup> TGG
R5XE001	GCGAAGGC	CCTGCTGGAA	CAT <sup>2</sup> ACTGAC	GCTGATGCCG	GAAAGC <sup>3</sup> TGG
R3XA001	GCGAAGGC	CCTGCTGGAA	CAT <sup>2</sup> ACTGAC	GCTGATGCCG	GAAAGC <sup>3</sup> TGG
R6XA001	GCGAAGGC	CCTGCTGGAA	CAT <sup>2</sup> ACTGAC	GCTGATGCCG	GAAAGC <sup>3</sup> TGG
R13D001INV	GCGAAGGC	CCTGCTGGAA	CAT <sup>2</sup> ACTGAC	GCTGATGCCG	GAAAGC <sup>3</sup> TGG
R27TOTAAL	GCGAAGGC	CCTGCTGGAA	CAT <sup>2</sup> ACTGAC	GCTGATGCCG	GAAAGC <sup>3</sup> TGG
R28TOTAAL	GCGAAGGC	CCTGCTGGAA	CAT <sup>2</sup> ACTGAC	GCTGATGCCG	GAAAGC <sup>3</sup> TGG
R2XA001	GG <sup>1</sup> AGCAAAAC	AGGATTAGAT	ACCC <sup>1</sup> GGTAG	TCCACGCCCT	AAACGATGGA
R5XE001	GG <sup>1</sup> AGCAAAAC	AGGATTAGAT	ACCC <sup>1</sup> GGTAG	TCCACGCCCT	AAACGATGGA
R3XA001	GG <sup>1</sup> AGCAAAAC	AGGATTAGAT	ACCC <sup>1</sup> GGTAG	TCCACGCCCT	AAACGATGGA
R6XA001	GG <sup>1</sup> AGCAAAAC	AGGATTAGAT	ACCC <sup>1</sup> GGTAG	TCCACGCCCT	AAACGATGGA
R13D001INV	GG <sup>1</sup> AGCAAAAC	AGGATTAGAT	ACCC <sup>1</sup> GGTAG	TCCACGCCCT	AAACGATGGA
R27TOTAAL	GG <sup>1</sup> AGCAAAAC	AGGATTAGAT	ACCC <sup>1</sup> GGTAG	TCCACGCCCT	AAACGATGGA
R28TOTAAL	GG <sup>1</sup> AGCAAAAC	AGGATTAGAT	ACCC <sup>1</sup> GGTAG	TCCACGCCCT	AAACGATGGA
R2XA001	TGCTAAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT <sup>2</sup> AGCT	AAGGCATTAA
R5XE001	TGCTAAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT <sup>2</sup> AGCT	AAGGCATTAA
R3XA001	TGCTAAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT <sup>2</sup> AGCT	AAGGCATTAA
R6XA001	TGCTAAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT <sup>2</sup> AGCT	AAGGCATTAA
R13D001INV	TGCTAAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT <sup>2</sup> AGCT	AAGGCATTAA
R27TOTAAL	TGCTAAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT <sup>2</sup> AGCT	AAGGCATTAA
R28TOTAAL	TGCTAAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT <sup>2</sup> AGCT	AAGGCATTAA
R2XA001	G <sup>2</sup> ATCCCGCC	TGGGGAGTAG	GATCGCAAGA	T <sup>2</sup> TAAAAC <sup>2</sup> TA	AAGGAATAGA
R5XE001	G <sup>2</sup> ATCCCGCC	TGGGGAGTAG	GATCGCAAGA	T <sup>2</sup> TAAAAC <sup>2</sup> TA	AAGGAATAGA
R3XA001	G <sup>2</sup> ATCCCGCC	TGGGGAGTAG	GATCGCAAGA	T <sup>2</sup> TAAAAC <sup>2</sup> TA	AAGGAATAGA
R6XA001	G <sup>2</sup> ATCCCGCC	TGGGGAGTAG	GATCGCAAGA	T <sup>2</sup> TAAAAC <sup>2</sup> TA	AAGGAATAGA
R13D001INV	G <sup>2</sup> ATCCCGCC	TGGGGAGTAG	GATCGCAAGA	T <sup>2</sup> TAAAAC <sup>2</sup> TA	AAGGAATAGA
R27TOTAAL	G <sup>2</sup> ATCCCGCC	TGGGGAGTAG	GATCGCAAGA	T <sup>2</sup> TAAAAC <sup>2</sup> TA	AAGGAATAGA
R28TOTAAL	G <sup>2</sup> ATCCCGCC	TGGGGAGTAG	GATCGCAAGA	T <sup>2</sup> TAAAAC <sup>2</sup> TA	AAGGAATAGA
R2XA001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAAAT <sup>2</sup> CG	AAGATACCGG
R5XE001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAAAT <sup>2</sup> CG	AAGATACCGG
R3XA001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAAAT <sup>2</sup> CG	AAGATACCGG
R6XA001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAAAT <sup>2</sup> CG	AAGATACCGG
R13D001INV	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAAAT <sup>2</sup> CG	AAGATACCGG
R27TOTAAL	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAAAT <sup>2</sup> CG	AAGATACCGG
R28TOTAAL	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAAAT <sup>2</sup> CG	AAGATACCGG

Figure 4 - 3

R2XA001	AAGAACCTTA	CCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGG
R5XE001	AAGAACCTTA	CCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGG
R3XA001	AAGAACCTTA	CCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGG
R6XA001	AAGAACCTTA	CCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGG
R13D001INV	AAGAACCTTA	CCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGG
R27TOTAAL	AAGAACCTTA	CCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGG
R28TOTAAL	AAGAACCTTA	CCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGG
R2XA001	GTGCCAGTTT	ACTGGAGCT	GAAACAGGT	GCTGCACGG	TGTCGTCAGC
R5XE001	GTGCCAGTTT	ACTGGAGCT	GAAACAGGT	GCTGCACGG	TGTCGTCAGC
R3XA001	GTGCCAGTTT	ACTGGAGCT	GAAACAGGT	GCTGCACGG	TGTCGTCAGC
R6XA001	GTGCCAGTTT	ACTGGAGCT	GAAACAGGT	GCTGCACGG	TGTCGTCAGC
R13D001INV	GTGCCAGTTT	ACTGGAGCT	GAAACAGGT	GCTGCACGG	TGTCGTCAGC
R27TOTAAL	GTGCCAGTTT	ACTGGAGCT	GAAACAGGT	GCTGCACGG	TGTCGTCAGC
R28TOTAAL	GTGCCAGTTT	ACTGGAGCT	GAAACAGGT	GCTGCACGG	TGTCGTCAGC
R2XA001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AAACCTCGTC
R5XE001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AAACCTCGTC
R3XA001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AAACCTCGTC
R6XA001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AAACCTCGTC
R13D001INV	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AAACCTCGTC
R27TOTAAL	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AAACCTCGTC
R28TOTAAL	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AAACCTCGTC
R2XA001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R5XE001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R3XA001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R6XA001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R13D001INV	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R27TOTAAL	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R28TOTAAL	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R2XA001	GGGAGGAGAA	GGCGAGGATG	ACGTCAAGTC	ATC	ATGGCC
R5XE001	GGGAGGAGAA	GGCGAGGATG	ACGTCAAGTC	ATC	ATGGCC
R3XA001	GGGAGGAGAA	GGCGAGGATG	ACGTCAAGTC	ATC	ATGGCC
R6XA001	GGGAGGAGAA	GGCGAGGATG	ACGTCAAGTC	ATC	ATGGCC
R13D001INV	GGGAGGAGAA	GGCGAGGATG	ACGTCAAGTC	ATC	ATGGCC
R27TOTAAL	GGGAGGAGAA	GGCGAGGATG	ACGTCAAGTC	ATC	ATGGCC
R28TOTAAL	GGGAGGAGAA	GGCGAGGATG	ACGTCAAGTC	ATC	ATGGCC
R2XA001	GGGCTACGC	ACGTGCTACA	ATGGGATGTA	CAAGAGAGATG	CAATGTCGTA
R5XE001	GGGCTACGC	ACGTGCTACA	ATGGGATGTA	CAAGAGAGATG	CAATGTCGTA
R3XA001	GGGCTACGC	ACGTGCTACA	ATGGGATGTA	CAAGAGAGATG	CAATGTCGTA
R6XA001	GGGCTACGC	ACGTGCTACA	ATGGGATGTA	CAAGAGAGATG	CAATGTCGTA
R13D001INV	GGGCTACGC	ACGTGCTACA	ATGGGATGTA	CAAGAGAGATG	CAATGTCGTA
R27TOTAAL	GGGCTACGC	ACGTGCTACA	ATGGGATGTA	CAAGAGAGATG	CAATGTCGTA
R28TOTAAL	GGGCTACGC	ACGTGCTACA	ATGGGATGTA	CAAGAGAGATG	CAATGTCGTA

Figure 4 - 4

R2XA001	AGATGGAGCA	AAACTCAAAA	ACATCTCCCA	GTTCGGATTG	TGGTCTGCA
R5XE001	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R3XA001	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R6XA001	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R13D001INV	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R27TOTAAL	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R28TOTAAL	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCGGATTG	TGGTCTGCA

R2XA001	CTCGACCACA	TG	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R5XE001	CTCGACCACA	TG	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R3XA001	CTCGACCACA	TG	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R6XA001	CTCGACCACA	TG	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R13D001INV	CTCGACCACA	TG	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R27TOTAAL	CTCGACCACA	TG	ATCTCCCA	GTTCGGATTG	TGGTCTGCA
R28TOTAAL	CTCGACCACA	TG	ATCTCCCA	GTTCGGATTG	TGGTCTGCA

R2XA001	GGTGAATAC	GTTCCTGGGT	CTTGTACTCA	CCAATCAC	1335
R5XE001	GGTGAATAC	GTTCCTGGGT	CTTGTACTCA	CCA...	1331
R3XA001	GG	GTTCCTGGGT	CTTGTACTCA	CCA...	1299
R6XA001	GG	GTTCCTGGGT	CTTGTACTCA	CCA...	1267
R13D001INV	GG	GTTCCTGGGT	CTTGTACTCA	CCA...	1236
R27TOTAAL	GG	GTTCCTGGGT	CTTGTACTCA	CCA...	1194
R28TOTAAL	GG	GTTCCTGGGT	CTTGTACTCA	CCA...	1172

Figure 4 - 5

	1						50
2BXA001	TGCAAGTCGA	ACGATGAAGC	CTAGCTTGCT	AGGTTTGA	GTGGCGCACC		
4AXA001	TGCAAGTCGA	ACGATGAAGC	CTAGCTTGCT	AGGTTTGA	GTGGCGCACC		
6W06001	.....	.....	.....	.....	GTGGCGCACC		
V14D001	.....	.....	.....	.....	GTGGCGCACC		
V19DINV001	.....	.....	.....	.....	GTGDHGCACC		
	51						100
2BXA001	GGTGAGTAA	GCATAGATGA	CATGCCCTTT	AGTTTGGAA	AGCCACTAGA		
4AXA001	GGTGAGTAA	GCATAGATGA	CATGCCCTTT	AGTTTGGAA	AGCCACTAGA		
6W06001	GGTGAGTAA	GCATAGATGA	CATGCCCTTT	AGTTTGGAA	AGCCACTAGA		
V14D001	GGTGAGTAA	GCATAGATGA	CATGCCCTTT	AGTTTGGAA	AGCCACTAGA		
V19DINV001	GGTGAGTAA	GCATAGATGA	CATGCCCTTT	AGTTTGGAA	AGCCACTAGA		
	101						150
2BXA001	AATGGTGAT	TAATACCAAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT		
4AXA001	AATGGTGAT	TAATACCAAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT		
6W06001	AATGGTGAT	TAATACCAAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT		
V14D001	AATGGTGAT	TAATACCAAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT		
V19DINV001	AATGGTGAT	TAATACCAAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT		
	151						200
2BXA001	AAAGGATTGC	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC		
4AXA001	AAAGGATTGC	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC		
6W06001	AAAGGATTGC	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC		
V14D001	AAAGGATTGC	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC		
V19DINV001	AAAGGATTGC	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC		
	201						250
2BXA001	CAAGGCTAT	GACGGGTATC	CGGCTTGAGA	GGGTGAGCGG	ACACACTGGA		
4AXA001	CAAGGCTAT	GACGGGTATC	CGGCTTGAGA	GGGTGAGCGG	ACACACTGGA		
6W06001	CAAGGCTAT	GACGGGTATC	CGGCTTGAGA	GGGTGAGCGG	ACACACTGGA		
V14D001	CAAGGCTAT	GACGGGTATC	CGGCTTGAGA	GGGTGAGCGG	ACACACTGGA		
V19DINV001	CAAGGCTAT	GACGGGTATC	CGGCTTGAGA	GGGTGAGCGG	ACACACTGGA		
	251						300
2BXA001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC		
4AXA001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC		
6W06001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC		
V14D001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC		
V19DINV001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC		
	301						350
2BXA001	TCAATGGGGG	AAACCCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT		
4AXA001	TCAATGGGGG	AAACCCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT		
6W06001	TCAATGGGGG	AAACCCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT		
V14D001	TCAATGGGGG	AAACCCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT		
V19DINV001	TCAATGGGGG	AAACCCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT		
	351						400
2BXA001	TTAGGATCGT	AAACTCCTTT	TGTAGAGAA	GATAATGACC	GTAATCAACC		
4AXA001	TTAGGATCGT	AAACTCCTTT	TGTAGAGAA	GATAATGACC	GTAATCAACC		
6W06001	TTAGGATCGT	AAACTCCTTT	TGTAGAGAA	GATAATGACC	GTAATCAACC		
V14D001	TTAGGATCGT	AAACTCCTTT	TGTAGAGAA	GATAATGACC	GTAATCAACC		
V19DINV001	TTAGGATCGT	AAACTCCTTT	TGTAGAGAA	GATAATGACC	GTAATCAACC		

Figure 5 - 1



	401				450
2BXA001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCGGTAAT	ACGGAGGGTG
4AXA001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCGGTAAT	ACGGAGGGTG
6W06001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCGGTAAT	ACGGAGGGTG
V14D001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCGGTAAT	ACGGAGGGTG
V19DINV001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCGGTAAT	ACGGAGGGTG
	451				500
2BXA001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	CGCGGAGGA
4AXA001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	CGCGGAGGA
6W06001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	CGCGGAGGA
V14D001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	CGCGGAGGA
V19DINV001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	CGCGGAGGA
	501				550
2BXA001	CAAGTCAGGT	GTG...AAATC	CTATG...CTT	AACCATAGAA	CTGCATTTGA
4AXA001	CAAGTCAGGT	GTG...AAATC	CTATG...CTT	AACCATAGAA	CTGCATTTGA
6W06001	CAAGTCAGGT	GTG...AAATC	CTATG...CTT	AACCATAGAA	CTGCATTTGA
V14D001	CAAGTCAGGT	GTG...AAATC	CTATG...CTT	AACCATAGAA	CTGCATTTGA
V19DINV001	CAAGTCAGGT	GTG...AAATC	CTATG...CTT	AACCATAGAA	CTGCATTTGA
	551				600
2BXA001	AACATATCC	CTGGAGTGT	GGGAGGTAG	TGGGAATCT	TGGTGTAGGG
4AXA001	AACATATCC	CTGGAGTGT	GGGAGGTAG	TGGGAATCT	TGGTGTAGGG
6W06001	AACATATCC	CTGGAGTGT	GGGAGGTAG	TGGGAATCT	TGGTGTAGGG
V14D001	AACATATCC	CTGGAGTGT	GGGAGGTAG	TGGGAATCT	TGGTGTAGGG
V19DINV001	AACATATCC	CTGGAGTGT	GGGAGGTAG	TGGGAATCT	TGGTGTAGGG
	601				650
2BXA001	GGTAAATCC	GTAGAGATCA	AGAGGATAC	CTATTG...CGA	AGGCGACCTG
4AXA001	GGTAAATCC	GTAGAGATCA	AGAGGATAC	CTATTG...CGA	AGGCGACCTG
6W06001	GGTAAATCC	GTAGAGATCA	AGAGGATAC	CTATTG...CGA	AGGCGACCTG
V14D001	GGTAAATCC	GTAGAGATCA	AGAGGATAC	CTATTG...CGA	AGGCGACCTG
V19DINV001	GGTAAATCC	GTAGAGATCA	AGAGGATAC	CTATTG...CGA	AGGCGACCTG
	651				700
2BXA001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
4AXA001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
6W06001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
V14D001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
V19DINV001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
	701				750
2BXA001	GATAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
4AXA001	GATAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
6W06001	GATAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
V14D001	GATAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
V19DINV001	GATAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
	751				800
2BXA001	GGGA...GGCTT	TGCTTTTCCA	GTAATGCAGG	TA...CGCCTTA	AGCATCCCGG
4AXA001	GGGA...GGCTT	TGCTTTTCCA	GTAATGCAGG	TA...CGCCTTA	AGCATCCCGG
6W06001	GGGA...GGCTT	TGCTTTTCCA	GTAATGCAGG	TA...CGCCTTA	AGCATCCCGG
V14D001	GGGA...GGCTT	TGCTTTTCCA	GTAATGCAGG	TA...CGCCTTA	AGCATCCCGG
V19DINV001	GGGA...GGCTT	TGCTTTTCCA	GTAATGCAGG	TA...CGCCTTA	AGCATCCCGG

Figure 5 - 2

	801				850	
2BXA001	CTGGGGAGTA	CGGTGCGAAG	ATTAAAACTC	AAARG	AATA	GACGGGGACC
4AXA001	CTGGGGAGTA	CGGTGCGAAG	ATTAAAACTC	AAAGG	AATA	GACGGGGACC
6W06001	CTGGGGAGTA	CGGTGCGAAG	ATTAAAACTC	AAARG	AATA	GACGGGGACC
V14D001	CTGGGGAGTA	CGGTGCGAAG	ATTAAAACTC	AAAGG	AATA	GACGGGGACC
V19DINV001	CTGGGGAGTA	CGGTCGCAAG	ATTAAAACTC	AAARG	AATA	GACGGGGACC
	851				900	
2BXA001	CGCACAAAGC	GTTGAGCATG	TGGTTTAATT	CGAGCTTACA		CGAAGAACC
4AXA001	CGCACAAAGC	GTTGAGCATG	TGGTTTAATT	CGAGCTTACA		CGAAGAACC
6W06001	CGCACAAAGC	GTTGAGCATG	TGGTTTAATT	CGAGCTTACA		CGAAGAACC
V14D001	CGCACAAAGC	GTTGAGCATG	TGGTTTAATT	CGAGCTTACA		CGAAGAACC
V19DINV001	CGCACAAAGC	GTTGAGCATG	TGGTTTAATT	CGAGCTTACA		CGAAGAACC
	901				950	
2BXA001	TTACCTTAGGC	TTGACATTG	AAGGAATTCG	C	PAGAAATA	GGGGAGTGTG
4AXA001	TTACCTTAGGC	TTGACATTG	AAGGAATTCG	C	PAGAAATA	GGGGAGTGTG
6W06001	TTACCTTAGGC	TTGACATTG	AAGGAATTCG	C	PAGAAATA	GGGGAGTGTG
V14D001	TTACCTTAGGC	TTGACATTG	AAGGAATTCG	C	PAGAAATA	GGGGAGTGTG
V19DINV001	TTACCTTAGGC	TTGACATTG	AAGGAATTCG	C	PAGAAATA	GGGGAGTGTG
	951				1000	
2BXA001	PAGTTTGCTA	GACCCGTGAA	ACAGGTGCTG	CACGGCTGTG	CTCAGCTCGT	
4AXA001	PAGTTTGCTA	GACCCGTGAA	ACAGGTGCTG	CACGGCTGTG	CTCAGCTCGT	
6W06001	PAGTTTGCTA	GACCCGTGAA	ACAGGTGCTG	CACGGCTGTG	CTCAGCTCGT	
V14D001	PAGTTTGCTA	GACCCGTGAA	ACAGGTGCTG	CACGGCTGTG	CTCAGCTCGT	
V19DINV001	PAGTTTGCTA	GACCCGTGAA	ACAGGTGCTG	CACGGCTGTG	CTCAGCTCGT	
	1001				1050	
2BXA001	GTCTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
4AXA001	GTCTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
6W06001	GTCTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
V14D001	GTCTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
V19DINV001	GTCTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
	1051				1100	
2BXA001	AGTTGCTAAG	AGGTTTATG	GCGCACTCTA	AGAAGACTGC	CTGGCTAAGG	
4AXA001	AGTTGCTAAG	AGGTTTATG	GCGCACTCTA	AGAAGACTGC	CTGGCTAAGG	
6W06001	AGTTGCTAAG	AGGTTTATG	GCGCACTCTA	AGAAGACTGC	CTGGCTAAGG	
V14D001	AGTTGCTAAG	AGGTTTATG	GCGCACTCTA	AGAAGACTGC	CTGGCTAAGG	
V19DINV001	AGTTGCTAAG	AGGTTTATG	GCGCACTCTA	AGAAGACTGC	CTGGCTAAGG	
	1101				1150	
2BXA001	AGGAGGAAGG	TGAGGACGAC	GTCAGTCA	CATGGCCCTT	ACGCCTAGGG	
4AXA001	AGGAGGAAGG	TGAGGACGAC	GTCAGTCA	CATGGCCCTT	ACGCCTAGGG	
6W06001	AGGAGGAAGG	TGAGGACGAC	GTCAGTCA	CATGGCCCTT	ACGCCTAGGG	
V14D001	AGGAGGAAGG	TGAGGACGAC	GTCAGTCA	CATGGCCCTT	ACGCCTAGGG	
V19DINV001	AGGAGGAAGG	TGAGGACGAC	GTCAGTCA	CATGGCCCTT	ACGCCTAGGG	
	1151				1200	
2BXA001	CTACACACGT	GCTACAATGC	GGTGCACAAA	GAGATGCAAA	GCCGCCGAGGC	
4AXA001	CTACACACGT	GCTACAATGC	GGTGCACAAA	GAGATGCAAA	GCCGCCGAGGC	
6W06001	CTACACACGT	GCTACAATGC	GGTGCACAAA	GAGATGCAAA	GCCGCCGAGGC	
V14D001	CTACACACGT	GCTACAATGC	GGTGCACAAA	GAGATGCAAA	GCCGCCGAGGC	
V19DINV001	CTACACACGT	GCTACAATGC	GGTGCACAAA	GAGATGCAAA	GCCGCCGAGGC	

Figure 5 - 3

	1201				1250
2BXA001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG
4AXA001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG
6W06001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG
V14D001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG
V19DINV001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG
	1251				1300
2BXA001	CCTGCATGAA	GCTGGAAATC	GCTAGTAAAT	CGCAAAATCA	GCTATGTTGC
4AXA001	CCTGCATGAA	GCTGGAAATC	GCTAGTAAAT	CGCAAAATCA	GCTATGTTGC
6W06001	CCTGCATGAA	GCTGGAAATC	GCTAGTAAAT	CGCAAAATCA	GCTATGTTGC
V14D001	CCTGCATGAA	GCTGGAAATC	GCTAGTAAAT	CGCAAAATCA	GCTATGTTGC
V19DINV001	CCTGCATGAA	GCTGGAAATC	GCTAGTAAAT	CGCAAAATCA	GCTATGTTGC
	1301				1350
2BXA001	GGTGAATAAC	GTTCGCCGGG	TCCTGTACTC	ACCGCCCCGT	CACACCATG
4AXA001	GGTGAATAAC	GTTCGCCGGG	TCCTGTACTC	ACCGCCCCGT	CACACCATG
6W06001	GGTGAATAAC	GTTCGCCGGG	TCCTGTACTC	ACCGCCCCGT	CACACCATG
V14D001	GGTGAATAAC	GTTCGCCGGG	TCCTGTACTC	ACCGCCCCGT	CACACCATG
V19DINV001	GGTGAATAAC	GTTCGCCGGG	TCCTGTACTC	ACCGCCCCGT	CACACCATG
	1351				1400
2BXA001	GGAGTTGTGCT	TTGCCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCACCGG
4AXA001	GGAGTTGTGCT	TTGCCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCACCGG
6W06001	GGAGTTGTGCT	TTGCCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCACCGG
V14D001	GGAGTTGTGCT	TTGCCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCACCGG
V19DINV001	GGAGTTGTGCT	TTGCCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCACCGG
	1401				1447
2BXA001	CACACACAGC	AGTTGGGGTG	AAGTCGTAAC	AAGGTAACCC	GGGCGGC
4AXA001	CACACACAGC	AGTTGGGGTG	.....	.....	.....
6W06001	CACACACAGC	AGTTGGGGTG	.....	.....	.....
V14D001	CACACACAGC	AGTTGGGGTG	.....	.....	.....
V19DINV001	CACACACAGC	AGTTGGGGTG	.....	.....	.....

Figure 5 - 4



European Patent  
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## EUROPEAN SEARCH REPORT

Application Number  
EP 99 87 0035

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION
X	PASTER ET AL.: "Phylogeny of <i>Helicobacter felis</i> sp. nov., <i>Helicobacter mustelae</i> , and related bacteria." INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, vol. 41, no. 1, January 1991 (1991-01), pages 31-38, XP002110981 * the whole document *	1-10	C12Q1/68 A61K31/70
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*The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 4 August 1999	Examiner Reuter, U
CATEGORY OF CITED DOCUMENTS			
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

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